



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179839

TO: Stephen Kapushoc
Location: REM/3A60/2C70
Art Unit: 1634
Wednesday, February 22, 2006
Case Serial Number: 10/785981

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518
BBOB
barbara.obryen@uspto.gov

Search Notes

*Swire CIP
requested working folder
2-23-06*

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STIC-Biotech/ChemLib

199839

From: Kapushoc, Stephen T.
Sent: Thursday, February 16, 2006 4:32 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search for 10/785,981

Please search SEQ ID NOs: 1, 2, 3, 4, 5 for application 10/785,981

Thanks,
Steve

Stephen Kapushoc
Art Unit 1634 - USPTO
Tel: 571-272-3312
Office: REM 3A60
Mailbox: REM 2C70

RECEIVED

FEB 16 2006

USPTO
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 3992.58 Seconds

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccgaaatactatgt.....tgcaaccatgaaatggtttgagt 660

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

Database : GenBmbl:
1: gb_ba: *
2: gb_n: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_dat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	650	100.0	1588	9	BC004067	Mus muscu	BC004067 Mus muscu
2	650	100.0	1754	9	BC005660	Mus muscu	BC005660 Mus muscu
3	650	100.0	1761	9	BC018485	Mus muscu	BC018485 Mus muscu
4	650	100.0	1771	9	BC092053	Mus muscu	BC092053 Mus muscu
5	650	100.0	1778	9	BC018223	Mus muscu	BC018223 Mus muscu
6	658.4	99.8	1736	9	BC004005	Mus muscu	BC004005 Mus muscu
7	658.4	99.8	1756	9	BC092276	Mus muscu	BC092276 Mus muscu
8	656.8	99.5	1760	9	BC095965	Mus muscu	BC095965 Mus muscu
9	656.8	99.5	1779	9	BC03069	Mus muscu	BC03069 Mus muscu
10	653.6	99.0	181014	9	AL840626	Mouse DNA	AL840626 Mouse DNA
11	647.2	98.1	1722	6	AX306117	Sequence	AX306117 Sequence
12	647.2	98.1	1722	9	MUSBFPU		MUSBFPU
C 13	629.6	95.4	145253	9	AC138173	Mus muscu	AC138173 Mus muscu
C 14	629.6	95.4	186564	9	AC119816	Mus muscu	AC119816 Mus muscu
C 15	628.2	95.2	214658	9	AC133509	R. norvegicus	AC133509 R. norvegicus
16	626.4	94.9	1714	9	RNEFLIA		RNEFLIA
17	626.4	94.9	1737	9	R.NEFLIA		R.NEFLIA
18	626.4	94.9	1746	9	BC091297	Rattus no	BC091297 Rattus no

ALIGNMENTS

19	626.4	94.9	1771	9	BC063162		
20	626.4	94.9	1775	9	BC072542	Rattus no	BC072542 Rattus no
21	626.4	94.9	182416	9	AC095724	Mus muscu	AC095724 Mus muscu
22	626.4	94.9	192528	9	AC124512	Mus muscu	AC124512 Mus muscu
23	626.4	94.9	233219	14	AC136572	Rattus no	AC136572 Rattus no
C 24	626.4	94.2	250880	9	AC102040	Mus muscu	AC102040 Mus muscu
C 25	625.4	94.8	136258	14	AC166149	Mus muscu	AC166149 Mus muscu
C 26	625.4	94.8	179573	14	AC166748	Mus muscu	AC166748 Mus muscu
C 27	625.4	94.8	208266	14	AC110913	Mus muscu	AC110913 Mus muscu
					X13661	Mouse mRNA	X13661 Mouse mRNA
					AC00406	Mus muscu	AC00406 Mus muscu
					AC154274	Mus muscu	AC154274 Mus muscu
					L10339	Rat elongat	L10339 Rat elongat
					AC145861	Pan trogl	AC145861 Pan trogl
					AC147556	Mus muscu	AC147556 Mus muscu
					AC134666	Mus muscu	AC134666 Mus muscu
					AC161170	Mus muscu	AC161170 Mus muscu
					AC100406	Mus muscu	AC100406 Mus muscu
					AC154479	Mus muscu	AC154479 Mus muscu
					D005222	Cricetulus	D005222 Cricetulus
					X62245	O. cuniculus	X62245 O. cuniculus
					X09823	Oryctolagus	X09823 Oryctolagus
					AC094797	Rattus no	AC094797 Rattus no
					AC134118	Rattus no	AC134118 Rattus no
					AC116224	Rattus no	AC116224 Rattus no
					AC154254	Mus muscu	AC154254 Mus muscu
					AC154774	Mus muscu	AC154774 Mus muscu
					AC127720	Rattus no	AC127720 Rattus no

RESULT 1	BC004067	LOCUS	BC004067	1588 bp mRNA	DEFINITION	Mus musculus eukaryotic translation elongation factor 1 alpha 1, mRNA (cDNA clone MGC:8209 IMAGE:3590965), complete cds.
		ACCESSION	BC004067		VERSION	BC004067.1 GI:13278545
		KEYWORDS			ORGANISM	Mus musculus (house mouse)
		SOURCE				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
		REFERENCE			AUTHORS	Strauberg R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemesh,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heih,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapek,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Tsohuvaki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., McKernan,K.J., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Worley,K.C., Malek,J.A., Gunaratne,P.H., McEwan,P.J., Abramson,R.D., Mullainay,S.J., Bosak,S.A., Richards,S., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmitz,J., Butterfield,Y.S., Krzywinski,M.I.I., Skalska,U., Smailus,D.E., Scherzer,A., Schein,J.E., Jones,S.J. and Marta,M.A.
		TITLE			JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		PUBLISHED			REFERENCE	2 (bases 1 to 1588) Director MGC Project.
		AUTHORS			TITLE	Direct Submission
		JOURNAL			JOURNAL	Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\$

Result No.	Score	Query	Match	Length	DB	ID	Description
1	650	100.0	1588	9	BC004067	Mus muscu	BC004067 Mus muscu
2	650	100.0	1754	9	BC005660	Mus muscu	BC005660 Mus muscu
3	650	100.0	1761	9	BC018485	Mus muscu	BC018485 Mus muscu
4	650	100.0	1771	9	BC092053	Mus muscu	BC092053 Mus muscu
5	650	100.0	1778	9	BC018223	Mus muscu	BC018223 Mus muscu
6	658.4	99.8	1736	9	BC004005	Mus muscu	BC004005 Mus muscu
7	658.4	99.8	1756	9	BC092276	Mus muscu	BC092276 Mus muscu
8	656.8	99.5	1760	9	BC095965	Mus muscu	BC095965 Mus muscu
9	656.8	99.5	1779	9	BC03069	Mus muscu	BC03069 Mus muscu
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12	647.2	98.1	1722	9	MUSBFPU		MUSBFPU
C 13	629.6	95.4	145253	9	AC138173	Mus muscu	AC138173 Mus muscu
C 14	629.6	95.4	186564	9	AC119816	Mus muscu	AC119816 Mus muscu
C 15	628.2	95.2	214658	9	AC133509	R. norvegicus	AC133509 R. norvegicus
16	626.4	94.9	1714	9	RNEFLIA		RNEFLIA
17	626.4	94.9	1737	9	R.NEFLIA		R.NEFLIA
18	626.4	94.9	1746	9	BC091297	Rattus no	BC091297 Rattus no

REMARK
COMMENT
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgbps-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web Site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimmwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.lilnl.gov>

Series: TPAK Plate: 11 Row: C Column: 21

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES**source**

1. /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="traron:10090"
 /clone="MGC:8209 IMAGE:3590965"
 /tissue type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
 /clone.lib="NCI CCAP_1u29"
 /lab_hstr="DBH10B"
 /note="vector: pCMV-SPORT6"
 1..1588

/gene="Befilial"
 /note="Synonyms: MGC18758, MGC27859, MGC7551, MGC8115, MGCS209"
 /db_xref="GeneID:13627"
 /db_xref="MGU:1096881"
 58..1446

/gene="Befilial"
 /codon_Start=1
 /product="eukaryotic translation elongation factor 1 alpha 1"
 /protein_id="AAH04067_1"
 /db_xref="GeneID:13278546"
 /db_xref="GeneID:13627"
 /db_xref="MGU:1096881"

/translation=MGRKPSFKAYWLDKLKAFERGKTFKTYVTTIIDAPGHDFIKKMTGTGSOAQDCAVLYVAAGYCEFEAGISNGQTEBHALLAYTLYVKGGIDKRMPSDKRKEBIVKSVTYIKGNPDTVAFVSPWFGWKVRKPGDGSASGFTLLEALDCILPPTDKPLPQDVYKIGGIVPUVGRVETSYKPKMVTFPAVNVNTTEVKSVNHEALSEALPQDGNYGFVNQVNSVDRRNVAQSKNDPPMEAGFTAGVII1NHPGQISAGTAFLVLDCTHACKFIDRSRGKLEDPKFLISGFTDAVLYDPMYGPKPMCVFSDPYPLGRPAVRDNRQTVAVGVTIRADVKQAGAKVTKSAQOKAQAK"

gene**CDS**

RESULT 2
 BC005660 LOCUS BC005660 1754 bp mRNA linear ROD 25-JUL-2005
 DEFINITION Mus musculus eukaryotic translation elongation factor 1 alpha 1, mRNA (cDNA clone MGCI:8115 IMAGE:358966), complete cds.
 ACCESSION BC005660 VERSION BC005660.1 GI:13542942
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCES (bases 1 to 1754)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemesh,C.M., Schulter,G.D., Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Sapey,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Yoshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmitz,J., Myers,R.M., Butterfield,Y.S., Krywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J., and Marrs,M.A.

Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12479912

ORIGIN

Query Match 100.0%; Score 650; DB 9; Length 1588;
 Best Local Similarity 100.0%; Pred. No. 6..6e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGACCGAGCATACTATGACCATCATGATGCCAGACAGACTCATCAA 60
 Db 298 GAGACCGAGCATACTATGACCATCATGATGCCAGACAGACTCATCAA 357

Qy 61 AACATGATTAAGGCAATCCAGGTGACTGTCCTGATGTTGCTGTGTT 120
 Db 358 AACATGATTAAGGCAATCCAGGTGACTGTCCTGATGTTGCTGTGTT 417

Qy 121 GGTGAATTGAGCTGATCTCCAAGAACGGCAGACCCGAGCATGTCCTGGCT 180

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 560.102 Seconds
 (without alignments)
 7853.391 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccgaaatactatgt.....tgccaccaatggcttgagt 660

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡ Maximum Match 100§ Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2004ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	660	100.0	660	14	AD289038		Adz89038 Pig growth
2	660	100.0	660	14	AD279331		Adz79331 Swine grow
3	660	100.0	660	14	ADZ7168		Adz77168 Pig growth
4	655	2	99.3	1722	10	ADF10645	Adf10645 Rat angio
5	647	2	98.1	1722	6	AB19778	Ab19778 Mouse 18C
6	621	6	94.2	1404	10	ADB38712	Adb38712 Toxicity-
7	621	6	94.2	1404	13	ADV41496	Adv41496 Rat cardi
C	8	581	6	88.1	1246	4	Aai12127 Probe #12
C	9	581	6	88.1	1246	4	Aab67206 Human foe
C	10	581	6	88.1	1246	4	Aai47423 Probe #16
C	11	581	6	88.1	1246	4	Aba49293 Human bre
C	12	581	6	88.1	1246	4	Aba34302 Probe #12
C	13	581	6	88.1	1246	4	Aak11382 Human bon
C	14	581	6	88.1	1246	4	Aak15648 Human bra
C	15	581	6	88.1	1246	4	Abs40975 Human liv
C	16	581	6	88.1	1246	5	Aai107827 Probe #78
C	17	581	6	88.1	1246	6	AB515387 Human gen
C	18	581	6	88.1	1389	12	Ado00457 Novel hum
C	19	581	6	88.1	1389	12	Adn98888 Novel hum

ALIGNMENTS

RESULT 1	
ID	AD289038
XX	standard; DNA; 660 BP.
AC	AD289038;
XX	
DT	28-JUL-2005 (first entry)
XX	
DE	pig growth factor I (GF I) gene, seq id 1.
XX	
KW	Growth; biochip; swine; hog raising; growth factor I; gene; db.
XX	
SU	Sus scrofa; Kagoshima Berkshire.
XX	
PN	US2005112597-A1.
XX	
PD	26-MAY-2005.
XX	
PF	26-FEB-2004; 2004US-00785981.
XX	
PR	24-NOV-2003; 2003KR-00083653.
XX	

(YEOJ/)	PA	(KIMC/)	PA	(KIMC/)	PA
LEE J.	PA	YEON E.	PA	YEON E.	PA
(LEEJ/)	PA	(YEOJ/)	PA	(YEOJ/)	PA
(SONG Y.	PA	(CHUNG K.	PA	(CHUNG K.	PA
(CHOK/)	PA	(CHUNG K.	PA	(CHUNG K.	PA
(KIMI/)	PA	(KIMI/)	PA	(KIMI/)	PA
(JINS/)	PA	(JIN S.	PA	(JIN S.	PA
(PARK/)	PA	(PARK S.	PA	(PARK S.	PA
(JUNG J.	PA	(JUNG J.	PA	(JUNG J.	PA
(LEE M.	PA	(LEE M.	PA	(LEE M.	PA
(KWON E.	PA	(KWON E.	PA	(KWON E.	PA
(CHO E.	PA	(CHO E.	PA	(CHO E.	PA
(CHOH/)	PA	(CHOH/)	PA	(CHOH/)	PA
(SHIN S.	PA	(SHIN S.	PA	(SHIN S.	PA
(NRMH/)	PA	(NRMH/)	PA	(NRMH/)	PA
(HONG Y.	PA	(HONG Y.)	PA	(HONG Y.)	PA
(HONG S.	PA	(HONG S.)	PA	(HONG S.)	PA
(KANG Y.	PA	(KANG Y.)	PA	(KANG Y.)	PA
(HAYY/)	PA	(HAYY/)	PA	(HAYY/)	PA

Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
1	650	100.0	1700	4	BC092292		BN092292 Mus musculus	
2	656	8	99.5	673	BM945443	UI-M-EMO-	CF78670 HESE3_101	
3	656	8	99.5	678	CX785670	UI-M-FDO-	CB248368 UI-M-HLO-	
4	656	8	99.5	710	6	BM945776	CF945776 UI-M-EMO-	
5	656	8	99.5	719	3	BM946759	BM946759 UI-M-EMO-	
6	656	8	99.5	746	3	BQ042422	UI-M-EMO-	
7	656	8	99.5	748	3	BQ042422	UI-M-EMO-	
8	656	8	99.5	749	3	CA322009	UI-M-FXO-	
9	656	8	99.5	755	5	BQ444687	UI-M-ER0-	
10	656	8	99.5	757	7	CP951596	UI-M-HLO-	
11	656	8	99.5	760	8	CP949906	CP949906 UI-M-HKO-	
12	656	8	99.5	764	3	BQ177933	UI-M-ER0-	
13	656	8	99.5	771	3	BQ177934	UI-M-ER0-	
14	656	8	99.5	808	5	BQ571059	UI-M-FBO-	
15	656	8	99.5	879	5	BUS15295	BUS1595 AGENCOURT	
16	656	8	99.5	926	6	CA97421	BQ922583 AGENCOURT	
17	656	8	99.5	928	8	CP945583	BM45587 AGENCOURT	
18	656	8	99.5	1111	3	BM455687	BM455687 AGENCOURT	
19	656	8	99.5	1145	3	BM461263	BM461263 AGENCOURT	
20	656	8	99.5	1153	5	BUS15235	BUS15235 AGENCOURT	
21	656	8	99.5	1733	4	AK081725	AK081725 Mus musculus	
22	656	8	99.5	1734	4	AK076696	AK076696 Mus musculus	

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 OM nucleic - nucleic search, using sw model
 Run on: February 20, 2006, 10:51:20 ; Search time 3910,41 Seconds
 (without alignments)
 7896-735 Million cell updates/sec

Title: US-10-785-981-1
 Perfect score: 660
 Sequence: 1 gagaccgaaatactatgt.....tgcaaccatgaagtttgagt 660
 Scoring table: IDENTITY_NUC Gapext 1.0
 Searched: 41078325 seqs, 23393541228 residues
 Total number of hits satisfying chosen parameters: 82156650
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0*, Maximum Match 10*

Listing first 45 summaries

RESULT 1

BC092292

LOCUS

DEFINITION

Mus musculus

mRNA

linear

HTC

IMAGE:50668840

containing frame-shift errors.

BC092292

VERSION

GI:62185631

HTC.

Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Murinae; Mus.

1 (bases 1 to 1700)

REFERENCE

AUTHORS

Strausberg, R.L.,

Feng, B.A.,

Grouse, L.H.,

Derge, J.G.,

Strain, R.J.,

Collins, F.S.,

Wagner, L.,

Shuler, G.D.,

Altschul, S.F.,

Zeeberg, B.,

Bustow, K.H.,

Schafer, C.P.,

Bhat, N.K.,

Hopkins, R.F.,

Jordan, H.,

Moore, T.,

Max, S.I.,

Wang, J.,

Hsieh, F.,

Diatchenko, L.,

Marusina, K.,

Farmer, A.A.,

Rubin, G.M.,

Hong, L.,

Stapleton, M.,

Soares, M.B.,

Bonaldo, M.F.,

Casavant, T.L.,

Scheetz, T.E.,

Brownstein, M.J.,

Usdin, T.B.,

Toshiyuki, S.,

Carninci, P.,

Prange, C.,

Raha, S.S.,

Loqueland, N.A.,

Peters, G.J.,

Abramson, R.D.,

Mulyahayati, S.J.,

Bosak, S.J.,

McEvany, P.J.,

McEvany, P.J.,

Richards, S.,

Kernan, K.J.,

Malek, J.A.,

Guraratne, P.H.,

Richards, S.,

Worley, K.C.,

Hale, S.,

Garcia, A.M.,

Gay, L.J.,

Hulyk, S.W.,

Villalon, D.K.,

Muzny, D.M.,

Sodergren, E.J.,

Lu, X.,

Gibbs, R.A.,

Fahey, J.,

Hellon, E.,

Kettman, M.,

Madan, A.,

Young, A.C.,

Shevchenko, Y.,

Bouffard, G.G.,

Blakesley, R.W.,

Touchman, J.W.,

Green, E.D.,

Dickson, M.C.,

Rodriguez, A.,

Grimwood, P.H.,

Schmutz, J.,

Myers, R.M.,

Butterfield, Y.S.,

Krzywinski, M.I.,

Skalaka, U.,

Smailus, D.E.,

Schnarach, A.,

Schein, J.B.,

Jones, S.J.,

and Marra, M.A.,

CONSRIM

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1700)

NIH MGC Project

Direct Submission

Submitted (01-APR-2005)

Gene Collection (MGCG)

Bethesda, MD 20892-2550, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Page 2

FEATURES	source	FEATURES	source
QY	cgabbs-mail.nih.gov	QY	GGAGATGCGAGTGCACAGCTGGAGCTTGATTGATCTACCAACTCTGT 480
Tissue Procurement: Gilbert Smith, Ph.D.	Contact: nisc_ngc@nigri.nih.gov/	Db	GGCGGTGCCAGTCACAGCTGCTGAGCTTGGATCCACCAACTCTGT 732
CDNA Library Preparation: Life Technologies, Inc.	AKhter,N., Ayelle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,	QY	CCAACTGACAGGCTCTGGACTCCCTCAGGATGCTATAATAATGGAGGCTTGGC 540
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)	Bleakley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,	Db	733 CCAACTGAAAGCTCTGGACTCCCTCAGGATGCTATAATAATGGAGGCTTGGC 792
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;	Dietrich,N.L., Granite,S., Guan,X., Gupca,J., Haghghi,P.,	QY	GGAGATGCGAGTGCACAGCTGGAGCTTGATTGATCTACCAACTCTGT 600
Web site: http://www.nisc.nih.gov/	Hansen,N., Ho,S.-L., Karins,E., Kwong,P., Laric,P., Legaspi,R.,	Db	GGCGGTGCCAGTCACAGCTGCTGAGCTTGGATCCACCAACTCTGT 852
Contact: nisc_ngc@nigri.nih.gov/	Maduro,Q.L., Masiello,C., Mastriani,B., Mastrian,S.D., McCloskey,J.C.,	QY	GCTCGAGTCATGTAACACTGAGTCAGAGCTGTGAATGACCATGAAGCTTGAGT 660
Series: IRXK Plate: 193 Row: 8	Mcdowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,	Db	853 GCTCGAGTCATGTAACACTGAGTCAGTCGTGTGAATGACCATGAAGCTTGAGT 912
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer Frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein	Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.	RESULT 2	
This clone has the following problem: frame shifted.		BM945443	673 bp mRNA EST 14-MAR-2002
Location/Qualifiers		LOCUS	UI-M-EM0-bvh-1-15-0-UI.r1 NIH_BMAP_EM0 Mus musculus cDNA Clone
1..1700	/organism="Mus musculus"	DEFINITION	IMAGE:5692190 5' mRNA sequence.
	/mol_type="mRNA"	ACCESSION	BM945443
	/strain="Czech II"	VERSION	BM945443.1
	/db_xref="Exxon:10090"	KEYWORDS	GI:19423028
	/clone="IMAGE:5068840"	SOURCE	Mus musculus (house mouse)
	/tissue type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
	/clone lib="NCI CGAP_Lu29"	REFERENCE	1 (bases 1 to 673)
	/lab host="DH10B"	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
	/note="vector: pcMV-SPORT6"	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
		JOURNAL	Unpublished (1999)
		COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgs@nih.gov Tissue Procurement: Dr. James Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
			This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
		Seq primer: PYX-5	http://image.llnl.gov
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		1.	1..673
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6"	
		/db_xref="Exxon:10090"	
		/clone="IMAGE:5692190"	
		/tissue type="whole brain"	
		/dev_stage="embryo 18.5 dpc"	
		/lab_host="DH10B (T1 phage resistant)"	
		/note="Organ: brain; Vector: PYX-Asci; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Leinon and Soares, Genome Research, 6:91-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into PYX-Asci vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACCACT. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH). Hemin Chin, Ph.D., program coordinator."	
			ORIGIN
QY	Query Match 100.0%; Best Local Similarity 100.0%; Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	1 GAGACCAGGAATAATCTATGACCATCATGATGCCGGACAGAACCTCATCAA 60
Db		253 GAGACCAGGAATAATCTATGACCATCATGATGCCGGACAGAACCTCATCAA 312	FEATURES
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Db		313 AACATGATACAGGCCACATCCAGGCTGCTGCTGCTGATTTCTGCTGGCT 372	
QY		121 GGGAATTGTAAGCTGTTGAAACAGCTGATTTCTCAACAAAATGGATTCCACCGAGCCA 180	
Db		373 GGGAATTGTAAGCTGTTGAAACAGCTGATTTCTCAACAAAATGGATTCCACCGAGCCA 432	
QY		181 TACACCCCTGGTGTGAAACAGCTGATTTCTCAACAAAATGGATTCCACCGAGCCA 240	
Db		433 TACACCCCTGGTGTGAAACAGCTGATTTCTCAACAAAATGGATTCCACCGAGCCA 492	
QY		241 CCATACAGTCAGAGAGATACAGGAAATCTGTTGAAAGGTCAACCTACATTAGAA 300	
Db		493 CCATACAGTCAGAGAGATACAGGAAATCTGTTGAAAGGTCAACCTACATTAGAA 552	
QY		301 ATGGCTTAACCTGACAGTAGCATGGTCAAGGATGCTGTTGAAATGGATTCCAACGAGCA 360	
Db		555 ATGGCTTAACCTGACAGTAGCATGGTCAAGGATGCTGTTGAAATGGATTCCAACGAGCA 612	
QY		361 ATGGCTGGAGCCAACTGCTTAATATGCTTGTGCAATTCTGTTGAAATGGATTCCAACGAGCA 420	
Db		613 ATGGCTGGAGCCAACTGCTTAATATGCTTGTGCAATTCTGTTGAAATGGATTCCAACGAGCA 672	

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OM nucleic - nucleic search, using sw model.

Run on: February 20, 2006, 11:15:29 ; Search time 161.946 Seconds
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 (without alignments)

Title: US-10-785-981-1
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Scoring table: IDENTITY NUC Gapext 1.0

Searched: 1303057 seqs, 880780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

RESULT 1
 US-09-023-655-1278
 ; Sequence 1278, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; ADDRESS: Incyte Pharmaceuticals, Inc.
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEX/FAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1278:
 ; REGISTRATION NUMBER: 37,071
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1506 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: 931097

SEQUENCES

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2	581.6	88.1	1506	3	US-09-949-016-204	Sequence 204, App	Sequence 204, App
3	581.6	88.1	1747	3	US-09-949-016-1833	Sequence 1833, App	Sequence 1833, App
4	581.6	88.1	1749	3	US-09-949-016-3699	Sequence 3699, App	Sequence 3699, App
5	581.6	88.1	1749	3	US-09-949-016-3700	Sequence 3700, App	Sequence 3700, App
6	581.6	88.1	5749	3	US-09-949-016-15441	Sequence 15441, A	Sequence 15441, A
7	581.6	88.1	5749	3	US-09-949-016-15442	Sequence 15442, A	Sequence 15442, A
8	580.0	87.9	1753	9	5225348-2	Patent No. 5225348	Patent No. 5225348
9	570.4	86.4	2128	2	US-08-371-377-16	Sequence 16, App	Sequence 16, App
10	570.4	86.4	2128	3	US-08-875-553D-22	Sequence 22, App	Sequence 22, App
11	562.4	85.2	1750	3	US-09-949-016-2972	Sequence 2972, App	Sequence 2972, App
12	562.4	85.2	1750	3	US-09-949-016-2973	Sequence 2973, App	Sequence 2973, App
13	562.4	85.2	5750	3	US-09-949-016-14714	Sequence 14714, A	Sequence 14714, A
14	562.4	85.2	5750	3	US-09-949-016-14715	Sequence 14715, A	Sequence 14715, A
c 15	458.4	69.5	546	3	US-09-385-982-466	Sequence 466, App	Sequence 466, App
c 16	423.4	64.2	1229	3	US-09-655-1068	Sequence 1068, App	Sequence 1068, App
c 17	420.6	63.7	1747	3	US-09-949-016-1948	Sequence 1948, App	Sequence 1948, App
c 18	401.6	60.8	533	3	US-09-328-111-469	Sequence 469, App	Sequence 469, App
c 19	371.4	56.3	601	3	US-09-949-016-22182	Sequence 22182, A	Sequence 22182, A
c 20	371.4	56.3	601	3	US-09-949-016-131604	Sequence 131604, A	Sequence 131604, A
c 21	371.4	56.3	601	3	US-09-949-016-131608	Sequence 131608, A	Sequence 131608, A
c 22	363	55.0	85963	3	US-09-614-221A-492	Sequence 492, App	Sequence 492, App
c 23	340.6	51.6	1377	3	US-09-174-768-3	Sequence 3, App	Sequence 3, App
c 24	339	51.4	1500	3	US-09-174-768-3	Sequence 284, App	Sequence 284, App

ALIGNMENTS

US-09-023-655-1278

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 Qy 61 AACATGATTACAGCCACATCCAGGCTGACTGCTGTTCTGCTGTCTGGCT 120
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 Db 594 ATTGGCTACACCCGAGACAGATAATGGATTCACATTAAGAAA 653
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 Db 894 GCTCCAGTCAACGTTACACGAACTAAATCTGTCGAATGCACTGAAGCTTGACT 953

RESULT 2

US-09-949-016-204
 Sequence 204, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 204
 LENGTH: 1506
 TYPE: DNA

RESULT 3

US-09-949-016-1833
 Sequence 1833, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1833
 LENGTH: 1747

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OM nucleic - nucleic search, using sw mode1.

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Title: US-10-785-981-1

Perfect score: 660

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Listing first 45 summaries

ALIGNMENTS

RESULT 1

US-10-785-981-1

; Sequence 1, Application US/10785981
 ; Publication No. US20050112597A1
 ; GENERAL INFORMATION;
 ; APPLICANT: CHULWOOK, KIM
 ; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
 ; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
 ; FILE REFERENCE: 3884-0120P
 ; CURRENT APPLICATION NUMBER: US/10/785_981
 ; CURRENT FILING DATE: 2004-06-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID: Nos: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 660
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire

US-10-785-981-1

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Description

Sequence 1, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 1601, A

Sequence 208, App

Sequence 1962, A

Sequence 11, Appli

Sequence 1278, App

Sequence 74, Appli

Sequence 74, Appli

Sequence 653, App

Sequence 653, App

Sequence 653, App

Sequence 242, App

Sequence 756, Appli

Sequence 76, Appli

Sequence 254, App

Sequence 65, Appli

Sequence 623, App

Sequence 75, Appli

Sequence 2840, App

Sequence 438, App

Sequence 38, Appli

Sequence 60, Appli

Sequence 166, App

Sequence 624, Appli

Sequence 22, Appli

Sequence 407, App

Sequence 130623, A

Sequence 11307, A

Sequence 130618, A

Sequence 45065, A

Sequence 45065, A

Sequence 38724, A

Sequence 38724, A

Sequence 3935, Ap

Sequence 2149, Ap

Sequence 27989, A

Sequence 11410, A

Sequence 11409, A

Sequence 19051, A

Sequence 26843, A

Sequence 466, App

Sequence 127, App

Sequence 4749, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	660	100.0	660	9 US-10-785-981-1	Sequence 1, Appli
4	657.4	99.6	1040	7 US-10-424-1599-16011	Sequence 1601, A
5	655.2	99.3	1722	6 US-10-316-253-208	Sequence 208, App
c	651.6	88.1	1246	3 US-0-864-761-19622	Sequence 1962, A
7	581.6	88.1	1494	8 US-10-416-330-11	Sequence 11, Appli
8	581.6	88.1	1506	7 US-10-641-643-1278	Sequence 1278, App
9	581.6	88.1	1696	6 US-10-374-979-74	Sequence 74, Appli
10	581.6	88.1	1696	7 US-10-182-936A-74	Sequence 74, Appli
11	581.6	88.1	1696	8 US-10-477-238A-653	Sequence 653, App
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13	581.6	88.1	1696	9 US-10-477-173-653	Sequence 653, App
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15	581.6	88.1	1720	8 US-10-278-698-756	Sequence 756, Appli
16	581.6	88.1	1833	7 US-10-231-956A-76	Sequence 76, Appli
17	581.6	88.1	1833	8 US-10-684-422-254	Sequence 254, App
18	581.6	88.1	1833	9 US-10-489-740-65	Sequence 65, Appli
19	581.6	88.1	1833	9 US-10-956-157-623	Sequence 623, App
20	581.6	88.1	1837	7 US-10-439-703-75	Sequence 75, Appli
c	581.6	88.1	1950	3 US-0-9-864-761-2840	Sequence 2840, App
22	581.6	88.1	3415	3 US-0-9-823-245A-438	Sequence 438, App
23	578.4	87.6	959	9 US-10-617-316-38	Sequence 38, Appli

RESULT 2
US-10-789-723-1
*; Sequence 1, Application US/10789723
; Publication No. US20050112602A1
; GENERAL INFORMATION
; APPLICANT: GYEONGSANGNAM-DO
; ATTORNEY OR AGENT: CHULWOOK, KIM
; TITLE OF INVENTION: cDNA chip for screening specific genes and analyzing their function in swine
; FILE REFERENCE: YL0P040109US
; CURRENT APPLICATION NUMBER: US/10/789,723
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: KR 2003-83651
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire*
US-10-789-723-1

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 Best Local Similarity 100.0%; Pred. No. 5e-208;
 Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GAGACCGAAATACTATGACCATTGATGCCGGACAGAACCTCATCAA 60
 Qy 61 AACATGATTACAGGCACTCCAGGTGACTGTGTCCTGATTGTGGT 120
 Db 61 AACATGATTACAGGCACTCCAGGTGACTGTGTCCTGATTGTGGT 120
 Qy 121 GGTGAATTGAAAGCTGTTATCCTGAAAGACCCGAGCATCTCTGGT 180
 Db 121 GGTGAATTGAAAGCTGTTATCCTGAAAGACCCGAGCATCTCTGGT 180
 Qy 181 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Db 181 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Qy 181 1 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Db 181 1 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Qy 241 CCATACAGTCAACCTGACACAGTAGGAAATTGTAGGAACTCATTAAGAA 300
 Db 241 CCATACAGTCAACCTGACACAGTAGGAAATTGTAGGAACTCATTAAGAA 300
 Qy 301 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360
 Db 301 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360

RESULT 3
US-10-786-052-1
*; Sequence 1, Application US/10786052
; Publication No. US2005011368A1
; GENERAL INFORMATION
; APPLICANT: GYEONGSANGNAM-DO
; ATTORNEY OR AGENT: CHULWOOK, KIM
; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
; FILE REFERENCE: 3884-0119P
; CURRENT APPLICATION NUMBER: US/10/786,052
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: KR 2003-83652
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire*
US-10-786-052-1

Query Match 100.0%; Score 660; DB 9; Length 660;
 Best Local Similarity 100.0%; Pred. No. 5e-208;
 Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGOCAGCAAATACTATGACCATTGATGCCGGACAGAACCTCATCAA 60
 Db 1 GAGOCAGCAAATACTATGACCATTGATGCCGGACAGAACCTCATCAA 60
 Qy 61 AACATGATTACAGGCACTCCAGGTGACTGTGTCCTGATTGTGGT 120
 Db 61 AACATGATTACAGGCACTCCAGGTGACTGTGTCCTGATTGTGGT 120
 Qy 121 GGTGAATTGAAAGCTGTTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 180
 Db 121 GGTGAATTGAAAGCTGTTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 180
 Qy 181 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Db 181 TACACCCCTGGTGTAAACAGCTGATTTGTTGCTCAACAAATTGATTC 240
 Qy 241 CCATACAGTCAACCTGACACAGTAGGAAATTGTAGGAACTCATTAAGAA 300
 Db 241 CCATACAGTCAACCTGACACAGTAGGAAATTGTAGGAACTCATTAAGAA 300
 Qy 301 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360
 Db 301 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360
 Qy 361 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360
 Db 361 ATGGGCTAACACCTGACACAGTAGGAAATTGTGGTGGCAATTCTGGT 360

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 504.283 Seconds
(without alignments)

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaacctaaatctatgt.....tgcacatgaaggcttgtgat 660

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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* 1	581.6	88.1	1389	8 US-10-821-234-696	Sequence 696, App
* 2	581.6	88.1	1837	8 US-10-947-249-133	Sequence 133, App
3	581.6	88.1	1837	12 US-11-000-688-278	Sequence 278, App
4	577.6	87.5	1804	12 US-11-156-527-118	Sequence 118, App
5	570.4	86.4	2128	8 US-10-828-033-22	Sequence 22, App
6	420.6	63.7	1748	12 US-11-124-367A-101	Sequence 101, App
7	420.6	63.7	1798	12 US-11-124-367A-100	Sequence 100, App
8	420.6	63.7	2595	12 US-11-124-367A-99	Sequence 99, App
C 9	411.6	62.3	576	6 US-09-925-065A-2861.0	Sequence 2861.0, A
C 10	411.6	62.3	1320	6 US-09-925-065A-5527.54	Sequence 5527.54,
C 11	401.4	60.8	599	6 US-09-925-065A-346340	Sequence 346340,
12	387.4	58.7	2656	12 US-11-102-026A-6	Sequence 6, Appl
13	334.4	50.6	918	12 US-11-102-026A-51	Sequence 51, Appl
14	328.8	49.7	199130	8 US-10-995-561-13233	Sequence 13233, A
15	313.8	47.5	1733	12 US-11-128-061-280	Sequence 280, App
16	313.8	47.5	1733	12 US-11-128-049-280	Sequence 280, App
C 17	292.8	44.4	606	6 US-09-925-065A-346340	Sequence 346340,
18	289.2	43.8	1601	12 US-11-010-239-64	Sequence 64, Appl
19	275.2	41.7	552	6 US-09-925-065A-865515	Sequence 865515,
20	254	38.5	965	8 US-10-750-185-30341	Sequence 30341, A

ALIGNMENTS

RESULT 1
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 ; Sequence 696, Application US/10821234
 ; Publication No. US2005025511A1
 ; GENERAL INFORMATION;
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10-821-234
 ; PRIORITY APPLICATION NUMBER: 2004-04-07
 ; PRIORITY FILING DATE: 2004-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_Genes Version 1.0
 ; SEQ ID NO: 696
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-821-234-696

Query Match 88.1%; Score 581.6; DB 8; Length 1389;
 Best Local Similarity 92.6%; Pred. No. 8.1e-166;
 Matches 611; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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 Db 241 GAGACAGCAAGTACTATGTGATCATTTGTGCCCCAGAACGAGCTTCAA 300
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 Db 301 AACATGATTACAGGCACATCCCGGGCAGACTGCTGTCCTGATTGTTGCTGTT 360
 QY 121 GTGTGATTGAAGCTGGTATCTCAAGACGCCAGATGCTCTCTGCT 180
 Db 361 GTGTGATTGAAGCTGGTATCTCAAGACGCCAGATGCTCTCTGCT 420
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 Db 421 TACACACTGGGTTGAAACAATTAATGATTCCACTGAGCA 480

Result No.	Score	Query	Match	Length	DB ID	Description
1	530	GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.	5929	4	AB025261	- AB025261 Sus scrofa
2	526.8	Copyright (c) 1993 - 2006 Biocceleration Ltd.	5866	4	AB025262	- AB025262 Sus scrofa
3	482	OM nucleic - nucleic search, using bw mode!	5987	4	AB059399	Bos tauru
4	477.2	Run on: February 20, 2006, 10:36:14 ; Search time 3205.16 Seconds (without alignments)	90.9	4	AB088166	Equus cab
5	470.8	9396.598 Million cell updates/sec	5982	4	BC022376	Homo sapi
6	470.8	Title: US-10-785-981-2	88.8	6	CS018093	Sequence
7	470.8	Perfect score: 530	1953	6	CS025608	Sequence
8	470.8	Sequence: 1 gctgactgtatcgggagaatc.....tagtgcattgtaaatccctgg 530	5925	6	CS119311	Sequence
9	470.8	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	5925	6	AF111785	Homo sapi
10	470.8	Searched: 5883141 seqs, 28421725653 residues	5925	8	CQ731010	Sequence
11	459.6	Total number of hits satisfying chosen parameters:	11766282	6	U32574	Oryctolagus cuniculus
12	450	Minimum DB seq length: 0	5988	6	AB025260	Sus scrofa
13	431.2	Maximum DB seq length: 20000000000	5932	4	AK220548	Mus musculus
14	424.4	Post-processing: Minimum Match 0%	4910	9	CR523587	Gallus gallus
15	424.4	Maximum Match 100%	1806	1	CQ733076	Sequence
		Listing first 45 summaries	5904	6	CS018091	Sequence
			6016	6	CS025606	Sequence
			6016	8	AF111783	Homo sapi
SUMMARIES						
% Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
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	5: gb_ov:*					linear MAM 26-JAN-2001
	6: gb_pat:*					complete cds.
	7: gb_ph:*					
	8: gb_pr:*					ACCESSION
	9: gb_ro:*					AB025261
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	13: gb_vl:*					KEYWORDS
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	15: gb_pl:*					SOURCE
						ORGANISM
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus
						REFERENCE
						1 (sites)
						AUTHORS
						Chikuni K., Tanabe R., Muroya S., and Nakajima I.
						TITLE
						Differences in molecular structure among the porcine myosin heavy chain-2a, -2x, and -2b isoforms
						JOURNAL
						Meat Sci 57, 311-317 (2001)
						2 (bases 1 to 5929)
						AUTHORS
						Chikuni K.
						TITLE
						Submitted (23-MAR-1999) Koichi Chikuni, National Institute of Animal Industry, Meat Science Laboratory;
						Nourin-kenkyu-danchi, P.O.box 5, Tsukuba, Ibaraki 305-0901, Japan
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						/codon_start=1
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						/protein_id="BA88214..1"
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						/translation="MSDQEAAIFGEEAPYLRKSEKERIEAQNKPDATKTSVFAVPKESFVKCTVQSREGKVTVKTEAGATLTVKEDQVFPMNPKPFDKIEDMMTHLHEPV

Page 2

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NAYOQMLTDRENOSLILITGESEASQNTKRTYQFATTAUTGCKKEPKRPMQGOT
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TDSAIDPLGFTSDERTSYKLTKAVMNGXLEKPKOKOREQABPDGTAEKAYLOG
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DTKQPKQFICVGLDIAEGFEDENSLSQLCINPNEFLQOFNAMHMFVIEQEYKCEG
JEWEFIDGMGLAECTLAEKPGMISLLEECMCPKATDSTSPKHLQYOHGLKSNNF
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PGAMBEELVHULRCNGVEGRICRGFSRILYADEKORYVUNLASYAPEGOFIDS
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OM nucleic - nucleic search, using sw mode.

Run on: February 20, 2006, 10:32:49 ; Search time 449.779 Seconds
 (without alignments)
 7853.391 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgtatcgggagaatc.....taggccattgaaatccctgg 530

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

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	13: geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	100.0	530	14 ADZ89039	Adz89039 Pig growth
2	530	100.0	530	14 ADZ79332	Adz79332 Swine growth
3	530	100.0	530	14 ADZ77169	Adz77169 Pig growth
4	470.8	88.8	5925	10 ADD29577	Add29577 Human tum
5	470.8	88.8	5925	14 ADM95930	ADM95930 cDNA encod
6	470.8	88.8	5925	14 ADX15796	ADX15796 DNA encod
7	470.8	88.8	5925	14 ADX25983	ADX25983 Novel cel
8	432.4	81.6	5874	5 AAS85420	AAS85420 DNA encod
9	424.4	80.1	6016	14 ADM95928	ADM95928 cDNA encod
10	424.4	80.1	6016	14 ADX15794	ADX15794 DNA encod
11	424.4	80.1	6016	14 ADX25985	ADX25985 Novel cel
12	424.6	79.5	6010	12 ADQ22038	ADQ22038 Human sof
13	421.6	79.5	6010	12 ADQ22007	ADQ22007 Human sof
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15	421.6	79.5	6010	12 ADQ17288	ADQ17288 Human ske
16	421.6	79.5	6016	4 AAH57390	AAH57390 Human ske
17	421.2	79.5	5595	14 ADX26120	ADX26120 Novel cel
18	416.4	78.6	5595	14 ADM95926	ADM95926 cDNA encod
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ALIGNMENTS

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AC			
XX			
DT 28-JUL-2005	(first entry)		
XX			
DE	Pig growth factor II (GF II) gene, seq id 2.		
XX			
KW	Growth; biochip; swine; hog raising; growth factor II; gene; ds.		
XX			
OS	Sub scrofa; Kagoshima Berkshire.		
XX			
PN	US2005112597-A1.		
XX			
PD	26-MAY-2005.		
XX			
PF	26-FEB-2004;	2004US-00785981.	
XX			
PR	24-NOV-2003; 2003KR-00083653.		
XX			
PA	(KIMC/)	KIM C.	
PA	(YEON/)	YEO J.	
PA	(LEEJ/)	LEE J.	
PA	(SONG/)	SONG Y.	
PA	(CHOK/)	CHO K.	
PA	(CHUN/)	CHUNG K.	
PA	(KIMI/)	KIM I.	
PA	(JINS/)	JIN S.	
PA	(PARK/)	PARK S.	
PA	(PARK/)	JUNG J.	
PA	(LEEEM/)	LEE M.	
PA	(KWON/)	KWON E.	
PA	(CHOE/)	CHO E.	
PA	(CHOH/)	CHO H.	
PA	(SHIN/)	SHIN S.	
PA	(NAMH/)	NAM H.	
PA	(HONG/)	HONG Y.	
PA	(HONG/)	HONG S.	
PA	(KANG/)	KANG Y.	
PA	(HAYY/)	HAY Y.	

PA	(ROU J/)	ROU J.	XX	RESULT 2
	(KWAC/)	KWACK S.		
PA	(CHOI/)	CHOI I.		
PA	(KIMB/)	KIM B.		
PI	Park S,	Yeo J., Lee J., Song Y., Cho K., Chung K., Kim I., Jin S;	XX	ID ADZ79332 standard; cDNA; 530 BP.
PI	Jung J., Lee M., Kwon E., Cho H., Shin S., Nam H;			
PI	Hong Y., Kang S., Ha Y., Rou J., Kwack S., Choi I., Kim B;			
WPI:	2005-403140/41.			
XX	Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.			Swine growth factor GB-II cDNA for cDNA chip diagnostic method.
XX				KW biochip; screening; EST; expressed sequence tag; probe; muscle; immobilization; gene expression; polymorphism; diagnosis; animal breeding; growth factor; ss.
XX				KW
XX				XX
XX				XX
XX				XX
PS	PS	PS	XX	Unidentified.
XX			XX	OS
CC	CC	CC	XX	XX
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CC	CC	CC	XX	PD 26-MAY-2005.
CC	CC	CC	XX	PP 27-FEB-2004; 2004US-00789723.
CC	CC	CC	XX	PR 24-NOV-2003; 2003KR-00083651.
CC	CC	CC	XX	PA (KIMC/ KIM C.
CC	CC	CC	XX	PA (YEOJ/ YEO J.
CC	CC	CC	XX	PA (LEEBJ/ LEE J.
CC	CC	CC	XX	PA (SONG/ SONG Y.
CC	CC	CC	XX	PA (CHON/ CHUNG K.
CC	CC	CC	XX	PA (KIMI/ KIM I.
CC	CC	CC	XX	PA (JINS/ JIN S.
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CC	CC	CC	XX	PA (KWON/ KWON E.
CC	CC	CC	XX	PA (CHOB/ CHO E.
CC	CC	CC	XX	PA (CHOB/ CHO H.
CC	CC	CC	XX	PA (SHIN/ SHIN S.
CC	CC	CC	XX	PA (NAMH/ NAM H.
CC	CC	CC	XX	PA (HONG/ HONG Y.
CC	CC	CC	XX	PA (HONG/ HONG S.
CC	CC	CC	XX	PA (KANG/ KANG Y.
CC	CC	CC	XX	PA (HA/ HA Y.
CC	CC	CC	XX	PA (ROU/ ROU J.
CC	CC	CC	XX	PA (KWAC/ KWACK S.
CC	CC	CC	XX	PA (CHOI/ CHOI I.
CC	CC	CC	XX	PA (KIMB/ KIM B.
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Db	1	1 GCTGACTGATCGGGAGAAATCAGTCATCTTAATCACCGAGAAATCGGGCAGGAAGAC 60	XX	PI Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S, Nam S, Shin S, Cho H, Hong Y, Choi I, Choi S, Choi T, Choi J, Park S, Jung J, Lee M, Kwon E, Cho B, Cho H, Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B.
Qy	61	61 TGTGAAACGAAAGCTTGTCACTTTCAGTTGCCAACATTGCCGTCACTGGGAAGGA 120	XX	PI Park S, Jung J, Lee M, Kwon E, Cho B, Cho H, Hong Y, Hong S, Kang Y, Ha Y.
Db	61	61 TGTGAAACGAAAGCTTGTCACTTTCAGTTGCCAACATTGCCGTCACTGGGAAGGA 120	XX	PI Hong Y, Hong S, Kang Y, Ha Y.
Qy	121	121 GAAGGGAGAACCTAATCTCTGGCAAATGCGGGAACTCTGGAAAGTCAATGTCG 180	XX	PA (ROU/ ROU J.
Db	121	121 GAAGGGAGAACCTAATCTCTGGCAAATGCGGGAACTCTGGAAAGTCAATGTCG 180	XX	PA (KWAC/ KWACK S.
Qy	181	181 CAACCCCTGTCGGCCTTGCAACGCAAGCCAGCTTCCACTGCTCTCTCG 240	XX	PA (CHOI/ CHOI I.
Db	181	181 CAACCCCTGTCGGCCTTGCAACGCAAGCCAGCTTCCACTGCTCTCTCG 240	XX	PA (KIMB/ KIM B.
Qy	241	241 CTTGGTAAATTCACTGAGATCCACTGGTACCACTGGGAAAGTCTGCTGACT 300	XX	PT
Db	241	241 CTTGGTAAATTCACTGAGATCCACTGGTACCACTGGGAAAGTCTGCTGACT 300	XX	New cDNA chip comprising a probe capable of detecting marker gene specifically expressed in the muscle and fat tissues of swine, a PT substrate, useful for screening and function analysis of swine genes.
Qy	301	301 CGAACATATCTCTGAGAAAGTCTGAGGAACTTCCACTGCTGAGGCTA 360	XX	PT
Db	301	301 CGAACATATCTCTGAGAAAGTCTGAGGAACTTCCACTGCTGAGGCTA 360	XX	New cDNA chip comprising a probe capable of detecting marker gene specifically expressed in the muscle and fat tissues of swine, a PT substrate, useful for screening and function analysis of swine genes.
Qy	361	361 CCACATTTTATCATGATCTGCTAACAGAACGAGCTTCCAGTCTCTCG 420	XX	PT
Db	361	361 CCACATTTTATCATGATCTGCTAACAGAACGAGCTTCCAGTCTCTCG 420	XX	New cDNA chip comprising a probe capable of detecting marker gene specifically expressed in the muscle and fat tissues of swine, a PT substrate, useful for screening and function analysis of swine genes.
Qy	421	421 CACCAACCATAATGACTACGGCCCTTGCAAGGGAGAGTCACTGCTCCAGAT 480	XX	PT
Db	421	421 CACCAACCATAATGACTACGGCCCTTGCAAGGGAGAGTCACTGCTCCAGAT 480	XX	New cDNA chip comprising a probe capable of detecting marker gene specifically expressed in the muscle and fat tissues of swine, a PT substrate, useful for screening and function analysis of swine genes.
Qy	481	481 TGATGACCAACGAGGCTGATGGCCACAGATAGTCATGAAATCCTGG 530	XX	PT
Db	481	481 TGATGACCAACGAGGCTGATGGCCACAGATAGTCATGAAATCCTGG 530	XX	New cDNA chip comprising a probe capable of detecting marker gene specifically expressed in the muscle and fat tissues of swine, a PT substrate, useful for screening and function analysis of swine genes.

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3140.18 Seconds
 (without alignments)

7896.735 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgtactgtatcgggaaatc.....tagggccattgaaatccgg 530

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : EST:
 1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_htc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gbb1:*

10: gb_gbb2:*

11: gb_gbb3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
-- 1	462.8	87.3	5667	11 DQ052205	DQ052205 Homo sapi
2	462.8	87.3	5667	11 DQ052206	DQ052206 Pan trogl
3	450	84.9	2674	4 AK041122	AK041122 Mus muscu
4	447.6	84.5	752	4 DA43235	DA43235 L1B4216-0
5	431.2	81.4	3339	4 AK029328	AK029328 Mus muscu
6	429.2	81.0	623	8 DN423128	DN423128 L1B4216-0
7	427.6	80.7	648	8 DN421412	DN421412 L1B4216-0
8	424.4	80.7	771	8 DN425844	DN425844 L1B4216-0
9	424.4	80.1	5820	11 DQ059772	DQ059772 Homo sapi
10	422.4	79.7	650	8 DN424241	DN424241 L1B4216-1
11	421.6	79.5	5814	11 DQ052207	DQ052207 Homo sapi
12	418	78.9	5814	11 DQ052208	DQ052208 Pan trogl
13	416.4	78.6	6062	4 HSMB02948	HSMB02948 Homo sapi
14	415.2	78.3	785	8 DQ423007	DQ423007 L1B4216-0
c 15	412.4	77.8	675	6 CD621454	CD621454 56028779J
16	398.8	75.2	710	8 DN421704	DN421704 L1B4216-0
17	374.8	70.7	817	8 CX901213	CX901213 JGI CA99
18	369	69.6	493	5 BU387960	BU387960 603858632
19	368.2	69.5	5805	11 DQ029773	DQ029773 Pan trogl
20	367.8	69.4	539	1 AW918573	AW918573 ESN349877
21	367	69.2	649	8 DN421699	DN421699 L1B4216-0
22	366.6	69.2	667	8 DN421346	DN421346 L1B4216-0

ALIGNMENTS

RESULT 1	DQ052205	5667 bp DNA linear GSS 02-JUN-2005
LOCUS	Homo sapiens MYH1 gene, VIRTUAL TRANSCRIPT, partial sequence.	
DEFINITION	Genomic survey sequence.	
DQ052205		
ACCESSION	DQ052205.1	GI:66905676
VERSION		
KEYWORDS	GSS.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarzhini; Hominoidea; Homo	
REFERENCE	1 (bases 1 to 5667)	
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Pledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.	
TITLE	Direct Submission (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
JOURNAL	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (er) PLoS Biol. 3 (6), e170 (2005)	
PUBLMED	15863325	
REFERENCE	2 (bases 1 to 5667)	
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Pledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.	
TITLE	Direct Submission (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
COMMENT		
FEATURES	Location/Qualifiers	
Source	1. .5667 /organism="Homo sapiens" /mol-type="genomic DNA" /chromosome="17" <1. .>5667 /gene="MYH1" /locus_tag="HC20221"	

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 Best Local Similarity 92.9%; Pred. No. 1..3e-125;
 Matches 485; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY	9	ATCGGGAGAATCAGTCTTAATCACCGGAGAATCCGGGAGGAAGACTGTGAAACA	68	gene	/db_xref="taxon: 9598"
Db	505	ATCGGGAGAATCAGTCTTAATCACCGGAGAATCCGGGAGGAAGACTGTGAAACA	565	ORIGIN	<1...>567
QY	69	CGAACCGTGTCATCGAFTCTGCAATTGCCATCTGGCTCAGTGTGAAAGGG 128	Query Match	87.3%	Score 462.8; DB 11;
Db	566	CCAAACGGTGTCATCGAATTGCCATCTGGCTCAGTGTGAAAGGG 625	Best Local Similarity	92.9%	DB 11; Pred. No. 1.3e-125;
QY	129	AACCTACTCTGGAAATAATCGGGGACTCTGGAAATCAACATTGAGT 188	Matches	485; Conservative	0; Mismatches 37; Indels 0; Gaps 0;
Db	626	AAGTTACTCTGGAAATAATCGGGGACTCTGGAAATCAATCGTGC 685	QY	9	ATCGGGAGAATCAGTCTTAATCACCGGAGAATCCGGGAGGAAGACTGTGAAACA 68
QY	189	TGCTCGAGGSCCTTGGCAAGACGCAACTCCCTCTGGTGTGAA 248	Db	506	ATCGGGAGAATCAGTCTTAATCACCGGAGAATCCGGGAGGAAGACTGTGAAACA 565
Db	686	TACTGGGGCTTGGCAAGCGGCAAGTGTGAA 745	QY	69	CGAACCGTGTCATCGAATTGCCATCTGGCTCAGTGTGAAAGGGAGGG 128
QY	249	AATTCATCAGGATCCACTTGGTACCTGGTACACTGGGAAGCTCCACATT 308	Db	566	CCAAACGGTGTCATCGAATTGCCATCTGGCTCAGTGTGAAAGGGAGGGAGG 625
Db	746	AATTCATCAGGATCCACTTGGTACCTGGTACACTGGGAAGCTCCACATT 805	QY	129	AACCTACTCTGGCAANTGAGGGACTCTGGAAAGTATGATCTCAGTGC 188
QY	309	ATCPTCTGAGAAGCTTAGTCAAGTCTTACGTTAACGGAGAAGCTCCACATT 368	Db	626	RAGTTACTCTGGCAANTGAGGGAGCTCTGGCAAGTATGATCTCAGTGC 685
Db	806	ATCTCTGAGAAGCTTACGTTAACGGAGAAGCTCCACATT 865	QY	189	TGCTCGAGGSCCTTGGCAAGACGCAACTCCCTCTGGCTTGTGAA 248
QY	369	TTTATCAGATCATGCTTAACAAGAGCCAGGTCAATGAAATGCTCTGATCACC 428	Db	686	TACTGGGGCTTGGCAAGCGGCAAGTGTGAAAGCTGGTACATGCACTTGTGAA 745
Db	866	TTAACAGAATGCTTAACAAGAGCCAGTCAATTGCTCTGATCACC 925	QY	249	AATTCATCAGGATCAGTGTGAAAGCTCCACATTGCTGAGTCACTGGGAGC 308
QY	429	ACCCATATGACTAGGCCCTCTGTCAGTCAAGGGGAGATCTGTGCCAGCATGTGAC 488	Db	746	AATTCATCAGGATCAGTGTGAAAGCTCCACATTGCTGAGTCACTGGGAGC 805
Db	926	ACCCATACGATTATGCCCTCTGTCAGTCAAGGGGAGATCTGCCAACATTGTGAC 985	QY	309	ATCTCTGAGAAGCTTAGTCAAGTCTTCCAGCTTAAGGGAGAAGCTTACACATT 368
QY	489	AAGCAGGGCTGATGCCACAGATAGTGCCTGAAATCTGG 530	Db	806	ATCTCTGAGAAGCTTAGTCACTGGTACTAGTGTGAAATGCTCTGATCACCCA 428
Db	986	AAGAGAGCTGATGCCATAGATAGTGCCTGAAATCTGG 1027	QY	369	TTTATCAGATCATGCTTAACAAGAGCCAGGTCAATGAAATGCTCTGATCACC 428
Db	986	AAGAGAGCTGATGCCATAGATAGTGCCTGAAATCTGG 1027	Db	866	TITATCAGATCATGCTTAACAAGAGCCAGATCTGATGAAATGCTCTGATCACC 925
RESULT 2			QY	429	ACCCATATGACTAGGCCCTCTGTCAGTCAAGGGGAGATCTGTGCCAGCTTGTGAC 488
DQ052206		DQ052206 5667 bp DNA linear GSS 02-JUN-2005	Db	926	ACCCATACGATTATGCCCTCTGTCAGTCAAGGGGAGATCTGTGAC 985
DEFINITION		Pan trogloblytes MYH1 gene, VIRTUAL TRANSCRIPT, Partial sequence, genomic survey sequence.	QY	489	AAGCAGGGCTGATGCCACAGATAGTGCCTGAAATCTGG 530
ACCESSION		D0052206	Db	986	AAGAGAGCTGATGCCATAGATAGTGCCTGAAATCTGG 1027
VERSION		GI:66905677	RESULT 3		
KEYWORDS			AK041122		
SOURCE			LOCUS		AK041122
ORGANISM		Pan trogloblytes (chimpanzee)	DEFINITION	Mus musculus adult male aorta and vein cDNA RIKEN full-length enriched library, clone:AK030084A17 product:TYPE 3 MYOSIN HEAVY CHAIN homolog [Rana pipiens], full insert sequence.	AK041122
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Burchontogires; Primates; Catarrhini; Hominidae; Pan.	ACCESSION	AK041122.1	AK041122.1
		1 (bases 1 to 5667)	VERSION	HTC; CAP trapper.	GI:26334226
REFERENCE		Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	KEYWORDS	Mus musculus (house mouse)	
AUTHORS		A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees	ORGANISM	Mus musculus	
JOURNAL		(er) PLoS Biol. 3 (6), E170 (2005)	REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Carninci,P. and Hayashizaki,Y.
PUBMED		15869325	AUTHORS	Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Carninci,P. and Hayashizaki,Y.
2 (bases 1 to 5667)			TITLE	High-efficiency full-length cDNA cloning	1
REFERENCE		Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	JOURNAL	Journal Meth. Enzymol. 303, 19-44 (1999)	10349636
AUTHORS		Direct Submission	PUBLISHED		
TITLE		Submitted (05-MAY-2005) Celera Genomics, 45 West Guide Drive, Rockville, MD 20850, USA	REFERENCE		
JOURNAL		This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	AUTHORS	Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
COMMENT		Location/Qualifiers	TITLE		
FEATURES		1. .5667 /organism="Pan trogloblytes"	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	11042159
source		/mol_type="genomic DNA"	PUBLISHED		

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OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 11:15:29 ; Search time 130.047 Seconds
(without alignments)

7244.353 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgtactgtatcgggagaatc.....taggccattgaaatccctgg 530

Scoring table: IDENTITY NUC Gapext 1.0

Searched: 1303057 seqs, 886780928 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

Database :	Issued Patents NA:*				Description			
No.	Score	Query	Match	Length	DB	ID	Description	
1	470.8	88.8	5925	3	US-09-949-016-5233	Sequence 5233, AP		
2	424.4	80.1	6016	3	US-09-949-016-1054	Sequence 1054, AP		
3	424.4	80.1	6016	3	US-09-949-016-2264	Sequence 2264, AP		
4	362.4	68.4	6011	3	US-09-949-016-3017	Sequence 3017, AP		
5	347.6	65.6	5992	3	US-09-949-016-546	Sequence 546, AP		
6	347.6	65.6	5992	3	US-09-949-016-2263	Sequence 2263, AP		
7	328.4	62.0	5661	3	US-09-949-105-2	Sequence 2, Appli		
8	308.1	58.1	6008	3	US-09-949-016-5058	Sequence 5058, AP		
9	144	27.2	6644	3	US-08-875-435B-5	Sequence 5, Appli		
10	141.4	26.7	5919	3	US-08-875-435B-2	Sequence 2, Appli		
11	141.2	26.6	6175	3	US-08-875-435B-1	Sequence 1, Appli		
12	141	26.6	5883	3	US-09-949-016-5001	Sequence 5001, AP		
13	139.2	26.3	5574	3	US-09-917-254-40	Sequence 40, Appli		
14	139.2	26.3	6861	3	US-09-949-016-1240	Sequence 1240, AP		
15	139.2	26.3	6861	3	US-09-949-016-1241	Sequence 1241, AP		
16	139.2	26.3	6861	3	US-09-949-016-1242	Sequence 1242, AP		
17	123.8	23.4	7596	3	US-09-023-655-1463	Sequence 1463, AP		
18	122.2	23.1	7453	3	US-09-620-312D-248	Sequence 248, AP		
19	109.4	20.6	3581	3	US-09-949-016-4965	Sequence 4965, AP		
20	105.2	19.8	28355	3	US-09-949-016-16975	Sequence 16975, A		
21	105	19.8	4668	3	US-09-949-016-4522	Sequence 4522, AP		
22	98.2	18.5	7501	3	US-09-620-312D-249	Sequence 249, AP		
23	94.6	17.8	30271	3	US-09-949-016-12796	Sequence 12796, A		
24	94.6	17.8	30272	3	US-09-949-016-14006	Sequence 14006, A		

ALIGNMENTS

RESULT 1
US-09-949-016-5233

; Sequence 5233, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY APPLICATION NUMBER: 2000-04-14
; CURRENT FILING DATE: 2000-10-20
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5233
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5233

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Best Local Similarity 93.0%; Pred: No. 7, 3e-140;
Matches 493; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GCTGACATCGGGAGAATCAGCTATTTAAATCCGGAGAATCCTGGGGCAGGAAGAC 60
Db 498 GCTGACATCGGGAGAATCAGCTATTTGATCAGTCACTGGCAGGAATCTGCAGGGAGAC 557
QY 61 TGTGAAACGAAACGGTTCATCCAGTACTTGCACATCGGGTACTGGGAGAAGA 120
Db 558 TGTGAAACCCAAAGGTTCATCCAGTACTTGAAACATTGGAGTACTGGGAGAAGA 617
QY 121 GAGGGAGAACCTACTCTGGAAATACTGGGAGATCAGTCACTGGCAGGGAGTC 180
Db 618 GAGGGAGAACGTTCTGGAAATACTGGGAGATCTGGAGATCAAATCATCGTGC 677
QY 181 CAACCCCTGCTGGCAAGCCAAAGCCTGAGAAACGACAATCCTCTCG 240
Db 678 CAACCCCTACTGGAGGGCTTGGCAAGGCCAGAACCTGAGAAATGACAACCTCTCG 737
QY 241 CTTGGTAATTCTACGAGATCCACTTGGTACCATCTGGAAAGCTGCTGAGAT 300

RESULT 3
US-09-949-016-2264
Sequence 104, Application US/09949016
PATENT NO. 6812339

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY NUMBER: 60/1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 2264
LENGTH: 6016
TYPE: DNA
ORGANISM: Human
US-09-949-016-2264

Query Match 80.1%; Score 424.4%; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125; Mismatches 66; Indels 0; Gaps 0;

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DB 609 GCTRACTGTGTTGAAACCTGTTGAAATCTGTTGATCTGTTGAGGAGAAC 668
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DB 669 TGTGACACAGAAGCTGTCACTCCAGTACTTGCCCAATTGCGGAAAGAA 728
QY 669 TGTGACACAGAAGCTGTCACTCCAGTACTTGCCCAATTGCGGAAAGAA 728
DB 789 TAACCCTCTACTGAAAGCTTCGCAATTGAGGGAACTTGGAAAGATCATCAGTC 180
QY 121 GAAAGGAAACCTACTCCGGCAAATGAGGGAACTTGGAAAGATCATCAGTC 180
DB 729 AAAAGGAAACCTGCTCTGGCAAATGGGGACCTCTGGAAATCATCAGTC 788
QY 181 CAACCCCCCTCTGGGCTTGGCAAGCCAAAGCTGGGAGAACACTCTCTCG 240
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QY 729 AAAAGGAAACCTGCTCTGGCAAATGGGGACCTCTGGAAATCATCAGTC 788
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QY 181 CAACCCCCCTCTGGGCTTGGCAAGCCAAAGCTGGGAGAACACTCTCTCG 240
DB 789 TAACCCCCCTACTGGAACTCTGGCAATGGGGAACTTGGAAAGATCATCAGTC 848
QY 301 CGAAACATATCTCTGAAAGTCTAGAAAGTCTAGAACTTCCGAAATGGGAAAGCTA 360
DB 909 TGAACATATCTGAACTGCTGAAAGTCTAGAAAGTCTAGAACTTCCGAAATGGGAAAGCTA 968
QY 361 CCACATTCTTCTGAACTGCTAATGAACTGCTGAAATGGCTCTGCTGCTG 420
DB 969 CCACATTCTTCTGAACTGCTAATGAACTGCTGAAATGGCTCTGCTGCTG 1028

QY 301 CGAAACATATCTCTGGAAATGGCTCTGAACTGCTAATGAACTGCTGCTG 420
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DB 1029 CCACATTCTTCTGAACTGCTAATGAACTGCTGCTGCTGCTG 1088

RESULT 2
US-09-949-016-1054
Sequence 104, Application US/09949016
PATENT NO. 6812339

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY NUMBER: 60/1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 1054
LENGTH: 6016
TYPE: DNA
ORGANISM: Human
US-09-949-016-1054

Query Match 80.1%; Score 424.4%; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125; Mismatches 66; Indels 0; Gaps 0;

QY 1 GCTGAAACAGAAGCTGTCACTCCAGTACTTGCACATCGCGTCACTGGGAGAAA 120
DB 669 TGTCACACAGAAGCTGTCACTCCAGTACTTGCACATCGCGTCACTGGGAGAAA 728
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QY 241 CTTGTGAAATTCTGAACTGCTCTGGTACCATCTGGTACCATCTGGCTCTG 300
DB 849 CTTGTGAAATTCTGAACTGCTCTGGTACCATCTGGCTCTG 908

QY 301 CGAAACATATCTCTGAAAGTCTAGAAAGTCTAGAACTTCCGAAATGGGAAAGCTA 360
DB 909 TGAACATATCTGAACTGCTGAAAGTCTAGAAAGTCTAGAAATGGCTCTGCTG 968
QY 361 CCACATTCTTCTGAACTGCTAATGAACTGCTGAAATGGCTCTGCTGCTG 420
DB 969 CCACATTCTTCTGAACTGCTAATGAACTGCTGCTGCTGCTG 1028

QY 301 CGAAACATATCTCTGGAAATGGCTCTGAACTGCTAATGAACTGCTGCTG 420
DB 909 TGAACATATCTGCTGAAAGTCTAGAAAGTCTAGAAAGTCTAGAAATGGCTCTGCTG 968
QY 361 CCACATTCTTCTGAACTGCTAATGAACTGCTGAAATGGCTCTGCTGCTG 420
DB 1029 CCACATTCTTCTGAACTGCTAATGAACTGCTGCTGCTGCTG 1088

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 641.579 Seconds
(without alignments)

6831.225 Million cell updates/sec

Title: US-10-785-981-2
Perfect score: 530
Sequence: 1 gctgactgtatcgggagaatc.....tagtgcattgaaatccctgg 530

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Sequence 22331, A

Sequence 27933, A

Sequence 47, Appl

Sequence 13, App

Sequence 859, Appl

Sequence 158, App

Sequence 48, Appl

Sequence 35, Appl

Qy 301 CGAACATATCTTCTAGAGAAGTCTAGAGTCACITCCAGCTAAAGGCCAAAGAGCTA 360
Db 301 CGAACATATCTTCTAGAGAAGTCTAGAGTCACITCCAGCTAAAGGCCAAAGAGCTA 360
Qy 361 CCACATTTTATCATGATCATGTCATAACAGAAAGCCTCATGGAAATGCTGT 420
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Qy 421 CACCAACCATAATGATGACTACGGCTTCTCAGTCAGGAGATCACITGCCAGCT 480
Db 421 CACCAACCATAATGATGACTACGGCTTCTCAGTCAGGAGATCACITGCCAGCT 480
Qy 481 TGATGACCTAACAGAGGAGCTGATGCCACAGATAGTGCCATTGAAATCCCTGG 530
Db 481 TGATGACCTAACAGAGGAGCTGATGCCACAGATAGTGCCATTGAAATCCCTGG 530

RESULT 3
US-10-786-052-2
; Sequence 2, Application US/10786052
; Publication No. US20050113568A1
; GENERAL INFORMATION:
; APPLICANT: CHULWOOK, KIM
; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
; FILE REFERENCE: 3884-0119P
; CURRENT APPLICATION NUMBER: US/10/786,052
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: KR 2003-83652
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire

US-10-786-052-2

Query Match 100.0%; Score 530; DB 9; Length 530;
Best Local Similarity 100.0%; Pred. No. 7, 6e-170;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGACTGATCGGAATCAGTCATCTTAATCACCGGAATTCGGCAGGAAGAC 60
Db 1 GCTGACTGATCGGAATCAGTCATCTTAATCACCGGAATTCGGCAGGAAGAC 60
Qy 61 TGTGAACACAGAACGGTGTCACTCCAGTACTCTGGCAATCAGCGTCACTGGGAGAGAA 120
Db 61 TGTGAACACAGAACGGTGTCACTCCAGTACTCTGGCAATCAGCGTCACTGGGAGAGAA 120
Qy 121 GAAGGGAAACCTACTCTGGAAATAGGGGACTCTGGAGATCAGATCATCGTCG 180
Db 121 GAAGGGAAACCTACTCTGGCAATAGGGGACTCTGGAGATCAGATCATCGTCG 180
Qy 181 CAACCCCCCTGCTCGAGCCCTTGGCAAACCCAAAGCCCTGGAGAACACTCTCTCG 240
Db 181 CAACCCCCCTGCTCGAGCCCTTGGCAAACCCAAAGCCCTGGAGAACACTCTCTCG 240
Qy 241 CTTTCGTAATTATCATCAGATTCAGATCCACTTCGGTACCATCTGGAAAGCTGGCTTCTGTGACAT 300
Db 241 CTTTCGTAATTATCATCAGATTCAGATCCACTTCGGTACCATCTGGAAAGCTGGCTTCTGTGACAT 300
Qy 301 CGAAACATATCTTCTAGAGTCTAGAGTCTAGACTCTTCAGCTAAAGGAAAGAGCTA 360
Db 301 CGAAACATATCTTCTAGAGTCTAGACTCTTCAGCTAAAGGAAAGAGCTA 360
Qy 361 CCACCCCAACCCTATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 420
Db 361 CCACCCCAACCCTATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 420
Qy 421 CACCCCAACCCTATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 480
Db 421 CACCCCAACCCTATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 480

RESULT 4
US-10-335-053-26
; Sequence 26, Application US/10335053
; Publication No. US20040241653A1

Qy 301 CGAACATATCTTCTAGAGTCTAGAGTCTAGGCACCTAACGGCAAAAGGCTA 360
Db 301 CGAACATATCTTCTAGAGTCTAGGCACCTAACGGCAAAAGGCTA 360
Qy 361 CACCAACCATAATGATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 420
Db 361 CACCAACCATAATGATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 420
Qy 421 CACCAACCATAATGATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 480
Db 421 CACCAACCATAATGATGACTACGGCTTCTGGAAAGCTGGCTTCTGTGACAT 480

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GenCore version 5.1.7

OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 11:27:30 ; Search time 404.955 Seconds
(without alignments)

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgtatcgggagaatc.....taggccattgaaatccctgg 530

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 144086446

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :	Published Applications NA_New.*			Description	OTHER INFORMATION: Description of Artificial sequences: primer
No.	Score	Query Match	Length	DB ID	FEATURE: NAME/KEY: misc_feature LOCATION: (1)-(5925) OTHER INFORMATION: myosin, heavy polypeptide 1, skeletal muscle, adult (MHC1) gene.
1	470.8	88.8	5925	12 US-11-000-688-1358	Sequence 1358, AP
2	416.4	78.6	6062	12 US-11-150-888-13	Sequence 13, APP1
3	345.8	66.6	6035	12 US-11-136-527-3751	Sequence 3751, AP
4	320.4	62.0	6021	12 US-11-136-527-274	Sequence 274, APP
5	301.6	57.3	5941	12 US-11-136-527-275	Sequence 275, APP
6	145.6	27.5	6060	12 US-11-136-527-2285	Sequence 2285, APP
7	145.6	27.5	6377	12 US-11-069-83-57	Sequence 57, APP1
8	144.2	27.4	7355	12 US-11-069-83-47	Sequence 47, APP1
9	144.8	27.3	6442	12 US-11-069-834-55	Sequence 55, APP1
10	144.2	27.2	6786	12 US-11-069-834-59	Sequence 59, APP1
11	141.2	26.6	7474	12 US-11-069-834-49	Sequence 49, APP1
12	139.2	26.3	6500	12 US-11-000-688-1142	Sequence 1142, APP
13	138.8	26.2	4239	8 US-10-995-561-148	Sequence 148, APP
14	138.8	26.2	6025	8 US-10-995-561-143	Sequence 143, APP
15	138.8	26.2	6148	8 US-10-995-561-147	Sequence 147, APP
16	138.8	26.2	6187	8 US-10-995-561-144	Sequence 144, APP
17	138.8	26.2	6886	8 US-10-995-561-149	Sequence 149, APP
18	138.8	26.2	6925	8 US-10-995-561-145	Sequence 145, APP
19	138	26.0	6185	8 US-10-995-561-146	Sequence 146, APP
20	135	25.5	2097	12 US-11-136-527-3099	Sequence 3099, AP

ALIGNMENTS

RESULT 1

; Sequence 1358, Application US-11000688

; Publication No. US20050287541

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, Francois

; APPLICANT: HOULGAUTE, Remi

; APPLICANT: BIRNBAUM, Daniel

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS

; FILE REFERENCE: 1423-R-03

; CURRENT APPLICATION NUMBER: US-11/000, 688

; PRIORITY APPLICATION NUMBER: US 60/525, 987

; PRIORITY FILING DATE: 2004-12-01

; NUMBER OF SEQ ID: NOS: 1596

; SEQ ID NO: 1358

; LENGTH: 5925

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial sequences: primer

; NAME/KEY: misc_feature

; LOCATION: (1)-(5925)

; OTHER INFORMATION: myosin, heavy polypeptide 1, skeletal muscle, adult (MHC1) gene.

US-11-000-688-1358

Query Match 88.8%; Score 470.8%; DB 12; Length 5925;

Best Local Similarity 93.0%; Pred. No. 7.2e-17;

Matches 493; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Db 498 GTGTGATCGTATCGGAGATCACTCTTAATCCGGAGATCCGGGAGTCAGTACTTGCCACAAATCGCGCTACTGGGAGAAGAA 557

Qy 61 TGTGAACAGAACGGGTGTCATCCAGTACTTGCCACAAATCGCGCTACTGGGAGAAGAA 120

Db 558 TGTGAACACCAAGCGTGTCACTCAGTACTTGCCACAAATCGCGCTACTGGGAGAAGAA 617

Qy 121 GAAGGAGAACCTACTCTGGAAAATGCGGGATCTGGAGATCATCATCATGTC 180

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.8	88.8	5925	12 US-11-000-688-1358	Sequence 1358, AP
2	416.4	78.6	6062	12 US-11-150-888-13	Sequence 13, APP1
3	345.8	66.6	6035	12 US-11-136-527-3751	Sequence 3751, AP
4	320.4	62.0	6021	12 US-11-136-527-274	Sequence 274, APP
5	301.6	57.3	5941	12 US-11-136-527-275	Sequence 275, APP
6	145.6	27.5	6060	12 US-11-136-527-2285	Sequence 2285, APP
7	145.6	27.5	6377	12 US-11-069-83-57	Sequence 57, APP1
8	144.2	27.4	7355	12 US-11-069-83-47	Sequence 47, APP1
9	144.8	27.3	6442	12 US-11-069-834-55	Sequence 55, APP1
10	144.2	27.2	6786	12 US-11-069-834-59	Sequence 59, APP1
11	141.2	26.6	7474	12 US-11-069-834-49	Sequence 49, APP1
12	139.2	26.3	6500	12 US-11-000-688-1142	Sequence 1142, APP
13	138.8	26.2	4239	8 US-10-995-561-148	Sequence 148, APP
14	138.8	26.2	6025	8 US-10-995-561-143	Sequence 143, APP
15	138.8	26.2	6148	8 US-10-995-561-147	Sequence 147, APP
16	138.8	26.2	6187	8 US-10-995-561-144	Sequence 144, APP
17	138.8	26.2	6886	8 US-10-995-561-149	Sequence 149, APP
18	138.8	26.2	6925	8 US-10-995-561-145	Sequence 145, APP
19	138	26.0	6185	8 US-10-995-561-146	Sequence 146, APP
20	135	25.5	2097	12 US-11-136-527-3099	Sequence 3099, AP

Result No.	Score	Query	Match	Length	DB ID	Description
1	528.4	89.7	1427	6	BD079915	BD079915 Cancer-associated sequence CQ721905
2	528.4	89.7	1677	6	CQ721905	CQ84036 Sequence AX077789 Sequence AK000759 Homo sapi AR336661 Sequence AC012488 Sequence AC012488 Homo sapi
3	528.4	89.7	1932	6	AC012488	AY116969 Homo sapi BC001243 Homo sapi AB169610 Macaca fa AB169783 Macaca fa
4	528.4	89.7	2357	6	AC012488	AB169783 Macaca fa AC155201 Callithri
5	528.4	89.7	2448	8	AC012488	AC155201 Callithri BD101385 Novel gene BD021447 Novel gene
6	528.4	89.7	2703	6	AC012488	GS7776 SHGC-103708 BC013617 Mus musculus AC153650 Mus musculus AC122925 Mus musculus
7	528.4	89.7	104089	8	AC012488	GS7776 SHGC-103708 BC013617 Mus musculus AC153650 Mus musculus AC122925 Mus musculus
8	526.8	89.4	1932	8	AY116969	AY116969 Homo sapi AB169610 Macaca fa AB169783 Macaca fa
9	526.8	89.4	2392	8	BC001243	AB169610 Macaca fa AB169783 Macaca fa
10	498	84.6	2445	8	AB169610	AB169610 Macaca fa AB169783 Macaca fa
11	498	84.6	2474	8	AB169783	AB169783 Macaca fa
12	466	79.1	184340	14	AC155201	AC155201 Callithri
13	353.8	60.1	776	6	BD101385	BD101385 Novel gene BD021447 Novel gene
14	353.8	60.1	776	6	BD021447	GS7776 SHGC-103708 BC013617 Mus musculus AC153650 Mus musculus AC122925 Mus musculus
c 15	317.8	54.0	517	10	GS7776	GS7776 SHGC-103708 BC013617 Mus musculus AC153650 Mus musculus AC122925 Mus musculus
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17	275	46.7	199753	9		
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/organism="Homo sapiens"	
/mol type="Genomic DNA"	
/db_xref="taxon:9606"	
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Qy 61 TCCAAATGCCCCACTTACAAGAGATACTTC Db 164 TCCAAATGCCCCACTTACAAGAGATACTTC	
Qy 121 GAGTAGATTCTGGCACTTCAATTGATGTCCTGAA Db 224 GAGTAGATTCTGGCACTTCAATTGATGTCCTGAA	
Qy 181 TTACCTAGGGTGAAGAACCTGACAGCAAATG Db 284 TTACCTAGGGTGAAGAACCTGACAGCAAATG	
Qy 241 ATATGTTGCAATTCTCTGTTCTGGGGCATTTGTC Db 344 ATATGTTGCAATTCTCTGTTCTGGGGCATTTGTC	
Qy 301 GTCATATTCTCTTGTAGACCAATTGTC Db 404 CGTCATATTCTCTTGTAGACCAATTGTC	
Qy 361 AGAACCATGCCAATCACCCTTAACAGAGAG Db 464 AGAACCATGCCAATCACCCTTAACAGAGAG	
Qy 421 CCTTCAGAAAGATTCTCTAAAGATGTTGCTGTT Db 524 CCTTCAGAAAGATTCTCTAAAGATGTTGCTGTT	
Qy 481 -TCAGTGACAGATCGAATCACAGGAGGG Db 584 GTTCAGTGACAGATCGAATCACAGGAGGG	
Qy 540 TGTATGCCAA 549 Db 644 CCTTCCCGAA 653	
RESULT 2 C0721905	
LOCUS C0721905 1677 bp	
DEFINITION Sequence 7839 from Patent WO0206868	
ACCESSION C0721905	
VERSION C0721905.1	
KEYWORDS GI:42282762	
SOURCE Homo sapiens (human)	
ORGANISM Homo sapiens	
Eudorypha; Metazoa; Chordata; Craniota; Mammalia; Eutheria; Eucharchontogli-	
Hominidae; Homo.	
REFERENCE 1. Venter, C.J., Adams, M.C., Li, P.W. AUTHORS	
TITLE	
JOURNAL	
FEATURES source	

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Query Match	89.7%	Score 528.4;	DB 6;	Length 1677;		
Best Local Similarity	98.7;	Pred. No. 9.2e-104;				
Matches	543;	Mismatches 0;				
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Qy	1	GTTGTCCTTAAATGATGTTGCCAACCTGATTGGAGACTCATTCAGAGTACCTAAGCTTCTTACATGATGATCACAA				
Db	466	GTTGTCCTTAAATGATGTTGCCAACCTGATTGGAGACTCATTCAGAGTACCTAAGCTTCTTACATGATGATCACAA				
Qy	61	TCAAATGGCCACCTAACAGAGATACTCAAGCTTCTTACATGATGATCACAA				
Db	526	TCAAATGGCCACCTAACAGAGATACTCAAGCTTCTTACATGATGATCACAA				
Qy	121	GAGTAATTCAAGAGTCATTGTCCTGAGTGTAGCAGTCAGAAACGTTG				
Db	596	GAGTAATTCAAGAGTCATTGTCCTGAGTGTAGCAGTCAGAAACGTTG				
Qy	181	TTACCTAGGGTAAACCTGACAGCAAATGAGTTGAAACCTGATGATGTTG				
Db	646	TTACCTAGGGTAAACCTGACAGCAAATGAGTTGAAACCTGATGATGTTG				
Qy	241	AATGGTGCACATTCTGTTTCTGGGGATTGATCCATGGTTATGCAACCCCT				
Db	706	AATGGTGCACATTCTGTTTCTGGGGATTGATCCATGGTTATGCAACCCCT				
Qy	301	CCTCATATTCCCTTAGATGAAACCATTGATCTTCTTAATGATGATCTT				
Db	766	CCTCATATTCCCTTAGATGAAACCATTGATCTTCTTAATGATGATCTT				
Qy	361	AAAGCATGCCAACTACTCCTTAACAGAAAGGGATAAACAGAAAGGG				
Db	826	AAAGCATGCCAACTACTCCTTAACAGAAAGGGATAAACAGAAAGGG				
Qy	421	CCCTCAGAGAAATTCTCTTAAAGATGTTGCTGCTGCTGAGTCCTTA				
Db	886	CCCTCAGAGAAATTCTCTTAAAGATGTTGCTGCTGCTGAGTCCTTA				
Qy	481	-TCACTGTACCAAGATCGAAATCACAGAAAGGGGGACTAAAGGAAC				
Db	946	GTCACTGTACCAAGATCGAAATCACAGAAAGGGGGACTAAAGGAAC				
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Db	1006	CTTCCCCCAA 10.15				
RESULT 3						
LOCUS	CQB48036	1932 bp	DNA	linear	PAT	
DEFINITION	Sequence 341	From Patent WO2004063362.				
ACCESSION	CQB48036					
VERSION	CQB48036..1	GI:51469572				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Buthidae; Euarchontoglires; Primates; Catarrhini; Hominoidea.					
FEATURES	1. 1932 AUTHORS Glover,D., Bell,G., Frenz,L. and Midgley,C. TITLE Cell cycle progression proteins JOURNAL Patent: WO 2004063362-A 341 29-JUL-2004; Cycloclase Limited (GB) Location/Qualifiers Source					
REFERENCE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="AK0001759"					
ORIGIN						

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OM nucleic - nucleic search, using sw model.

Run on: February 20, 2006, 10:51:20 ; Search time 3489,74 Seconds
 (without alignments)

Title: US-10-785-981-3
 Perfect score: 589
 Sequence: 1 gttgttcctttaatcatgt.....tagtccattgaaatccctgg 589

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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		FEATURES	source	
Qy	1 GTGTCCTTAATATGTGTGCCAACGTCATGGAGCTTGCATAATT 60			was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Db	40 GTGTCCTTAATATGTGTGCCAACGTCATGGAGCTTGCATAATT 99			Location/Qualifiers
Qy	61 TCCAATGTCACCTACAGAGAGATACTCAACTCTTACTGTGATCACATGAG 120			1. -1213
Db	100 TCCAATGTCACCTACAGAGAGATACTCAACTCTTACTGTGATCACATGAG 159			/organism="Homo sapiens"
Qy	121 GAACTAATCAGCAGTTCAATTGATGTCAGTCAGAACGTCCTCTGCT 180			/mol type="mRNA"
Db	160 GAACTAATCAGCAGTTCAATTGATGTCAGTCAGAACGTCCTCTGCT 219			/db_xref="taxon:9606"
Qy	181 TTACCTAGGATAAACCTGACAGCAATTGAAAGTTGATAGGAAGCA 240			/clones="CSODD004YK21"
Db	220 TTACCTAGGATAAACCTGACAGCAATTGATGTCAGTCAGAACGTCCTCTGCT 279			/tissue="Neuroblastoma Cot 50-normalized"
Qy	241 AATGTTGCAATCCCTGTTCTGGGGCATGATGATCCATGTTATGCCAACCTTGTCTGAC 300			/plasmid="pcMVSSPORT_6"
Db	280 AATGTTGCAATCCCTGTTCTGGGGCATGATCCATGTTATGCCAACCTTGTCTGAC 339			ORIGIN
Qy	301 CGTCATATTCCTTAGATGAACTAACCTGATCTCTTAATGTCAGTCATCTAGTCGAA 360			Query Match
Db	340 CGTCATATTCCTTAGATGAACTAACCTGATCTCTTAATGTCAGTCATCTAGTCGAA 399			Best Local Similarity
Qy	361 AGACCATGCAACTACCTTAAAGAGGGATAAACGAAAAATAATGTGAATA 420			Matches
Db	400 AGACCATGCAACTACCTTAAAGAGGGATAAACGAAAAATAATGTGAATA 459			543; Conservative
Qy	421 CCTTCAGAAAGAAATTCTCTAAAGATGTTGCTGCTGAGCTCTAAATAACAT 480			0; Mismatches
Db	460 CCTTCAGAAAGAAATTCTCTAAAGATGTTGCTGCTGAGCTCTAAATAACAT 519			6; Indels
Qy	481 -TCAGTGTACAGATCGAAATCACAGGAAGGGGGACTAAAGGAACTACAAAGCTGTTAGC 539			1; Gaps
Db	520 GTCACTGTACAGATCGAAATCACAGGAAGGGGGACTAAAGGAACTACAAAGCTGTTAGC 579			
Qy	540 TGATGACCAA 549			
Db	580 CCTTCGGAA 589			
RESULT 2				
CR621606	CR621606 1213 bp mRNA linear HTC 21-JUL-2004			RESULT 3
LOCUS				CR621025
DEFINITION	full-length cDNA clone CSODD004YK21 of Neuroblastoma Cot			1415 bp mRNA linear
	50-normalized of Homo sapiens (human).			clone CSODC023YH23 of Neuroblastoma Cot
ACCESSION				HTC 21-JUL-2004
VERSION	CR621606			
KEYWORDS	CR621606_1 GI:50502413			
SOURCE	HTC; CNSLT cDNA.			
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 1213)			
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.			
JOURNAL	Full-length cDNA libraries and normalization			
REMARK	Unpublished			
	Contact : Feng Liang Email : fliang@lifetech.com URL :			
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
	Faraday Avenue			
	2 (bases 1 to 1213)			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

Page 1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
MM nucleic - nucleic search, using SW model
run on: February 20, 2006, 10:32:49 ; Search time 499.848 Seconds
(without alignments)
7853.391 Million cell updates/sec
Title: US-10-785-981-3
Effect score: 589
Sequence: 1 gttgttccttaatatgat.....tagtggccattggaaatccctgg 589
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%

ALIGNMENTS

CONTINUED

result	Query			DB	ID	Description
	No.	Score	Match Length			
1	589	100.0	589	14	ADZ89040	Adz89040 Pig grow
2	589	100.0	589	14	ADZ89333	Adz79333 Swine gr
3	589	100.0	589	14	ADZ77170	Adz77170 Pig grow
4	528.4	89.7	1427	2	AAX40181	Aax40181 Lung canc
5	528.4	89.7	1932	13	ADQ99911	Adq89911 Antagoni
6	528.4	89.7	2357	4	AAF60005	Aaf86005 Human syn
7	528.4	89.7	2414	6	ABL89366	Abi89366 Human pol
8	528.4	89.7	2703	4	AAI58275	Aai58275 Human pol
9	528.4	89.7	2703	5	ADQ8482	Adq8482 DNA encod
10	528.4	89.7	2703	9	ADB48242	Adb48242 Novel hum
11	528.4	89.7	6499	4	AAK86748	Aak86748 Human immu
12	526.8	89.4	2451	10	ADI40392	Adi40392 Human pu
13	517.4	87.8	2410	4	AAI60061	Aai60061 Human pol
14	474.8	80.6	610	14	ACI57351	aci57351 Human co
15	391.6	66.5	2734	5	AA84422	Aa84422 DNA encod
16	353.8	60.1	776	4	AAI97610	Aai97610 Human neu
17	137	23.3	396	4	AAFP94959	Aaf94959 Human ova
18	137	23.3	396	6	ABL48309	Abi48309 Ovarian C
19	137	23.3	396	6	ART03226	Art03226 Human ovary

PA	(ROUJ/)	ROU J.	QY	541	GATGACCAAGAGGGCTGTGGCCAAGATACTGCATTAATCCTGG 589
PA	(KWA/C/)	KWACK S.	Db	541	GATGACCAAGAGGGCTGTGGCCAAGATACTGCATTAATCCTGG 589
PA	(CHOI/)	CHOI I.			
PA	(KIMB/)	KIM B.			
XX					
PI	Kim C,	Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;	RESULT 2		
PI	Park S,	Jung J, Lee M, Kwon B, Cho E, Cho H, Shin S, Nam H;	ID ADZ79333		
PI	Hong Y,	Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;	ADZ79333 standard		
XX	DR	XX	ID ADZ79333		
XX	WPI: 2005-403340/41.	XX	AC		
XX	Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.	DT 28-JUL-2005 (first entry)	DT		
XX	Claim 2; SEQ ID NO 3: 8pp; English.	XX	DE		
XX	The invention relates to a functional cDNA chip (I) for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises a probe comprising growth specific gene in muscle and fat tissues of swine, and a substrate on which the probe is immobilized. Further disclosed is a kit (K1) useful for screening and functional analysis of growth specific gene according to breeds and tissues of swine, comprising (I) integrated in it, Cy5-dCTP or Cy3-dCTP bound cDNA from RNA of the tissue to be screened, a fluorescence scanning system, and a computer analysis system (II) and (K1) are useful for screening and function analysis of growth specific gene according to breeds and tissues of swine. (I) is useful in the swine improvement and breeding of a new breed, and in the hog raising industry. The current sequence represents the pig growth factor III (GP III) gene.	XX	DF		
XX	Sequence 589 BP; 187 A; 110 C; 129 G; 163 T; 0 U; 0 Other;	XX	XX		
XX	Query Match 100.0%; Score 589; DB 14; Length 589;	XX	XX		
Best Local Similarity 100.0%; Pred. No. 4 9e-151;	Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX		
QY	1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60	QY	1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60	QY	1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60
Db	.1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60	Db	.1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60	Db	.1 GTTGTTCCTTAAATATGATGTTGCCACAGCTGCAATGGAGACTCATTCATTGCACTTAATATT 60
QY	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120	QY	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120	QY	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120
Db	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120	Db	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120	Db	61 TCCAAATGTCGACCTTACAAGAGATACTCAAGCTCTTCTTAATGATGATCACATGAG 120
QY	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180	QY	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180	QY	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180
Db	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180	Db	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180	Db	121 GAAGTAATTGCACTTCAATTGATGTCCTGAGTCTAGTGTAGCAAACTGTTCTGTGT 180
QY	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240	QY	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240	QY	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240
Db	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240	Db	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240	Db	181 TTACCTTAGGATAAAAACCTGACACCAAATGAAAGCTTGTAAACCTGAGTAAAGGA 240
QY	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300	QY	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300	QY	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300
Db	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300	Db	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300	Db	241 AATGTTGCAATCCGTGTTCTGGGGCATGTATCCATGATCTTATGCAACCTCTGCTGC 300
QY	301 CGTCATATCCTTATGATGACCAATTGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360	QY	301 CGTCATATCCTTATGATGACCAATTGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360	QY	301 CGTCATATCCTTATGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360
Db	301 CGTCATATCCTTATGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360	Db	301 CGTCATATCCTTATGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360	Db	301 CGTCATATCCTTATGATGACCACTGATCTTCAATGCTTCTAGTCAGA 360
QY	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420	QY	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420	QY	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420
Db	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420	Db	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420	Db	361 AAGACCATGCCAACATCCATTAAAGATGTTCTGGGGCATGTATCCATGATCTTATGCA 420
QY	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480	QY	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480	QY	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480
Db	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480	Db	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480	Db	421 CCTTCAGAAAGATTCTCAATTGATGTTCTGGGGCATGTATCCATGATCTTATGCA 480
QY	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540	QY	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540	QY	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540
Db	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540	Db	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540	Db	481 TCAGGTGTCAGATCAATCACAGGAAGGGGACTAAAGGAACACTACAGCTGTTAGGT 540

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 144.524 Seconds
(without alignments)
7244.353 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttcctttaatatgtat.....tagggccattgaaatccctgg 589

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780928 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1	528.4	89.7	2703	3	US-09-620-312D-152		Sequence 152, App
2	137	23.3	396	3	US-09-640-173-150		Sequence 150, App
3	137	23.3	396	3	US-09-713-550-150		Sequence 150, App
4	137	23.3	396	3	US-09-825-294-150		Sequence 150, App
5	137	23.3	396	3	US-09-970-966-150		Sequence 150, App
6	48.2	8.2	886	3	US-09-270-767-151527		Sequence 15199, A
7	48.2	8.2	1514	3	US-09-270-767-15199		Sequence 22, App
8	48	8.1	1141	3	US-09-806-708B-22		Sequence 5233, AP
9	43.6	7.4	5925	3	US-09-949-016-5233		Sequence 1054, AP
10	40.4	6.9	6016	3	US-09-949-016-1054		Sequence 2264, AP
11	40.4	6.9	6016	3	US-09-949-016-2264		Sequence 2264, AP
12	39.4	6.7	1428	3	US-09-248-796A-1936		Sequence 1936, AP
c 13	39.4	6.7	2082	3	US-09-248-796A-2564		Sequence 2564, AP
14	38.8	6.6	601	3	US-09-949-016-40750		Sequence 40750, A
c 15	38.8	6.6	462589	3	US-09-949-016-12900		Sequence 12900, A
c 16	38.8	6.6	476044	3	US-09-949-016-12412		Sequence 12412, A
c 17	38.6	6.6	723	3	US-09-134-000C-2397		Sequence 2397, AP
c 18	38.4	6.5	9048	3	US-08-973-273-4		Sequence 4, App
c 19	38.2	6.5	1368	3	US-09-248-796A-11323		Sequence 11323, A
20	38.2	6.5	1716	3	US-08-656-034-9		Sequence 9, App
21	37.8	6.5	1698	3	US-09-248-796A-1623		Sequence 1623, AP
c 22	37.8	6.4	822	3	US-09-710-279-607		Sequence 607, AP
c 23	37.8	6.4	2950	3	US-09-710-279-3349		Sequence 3349, AP
c 24	37.8	6.4	3760	3	US-09-710-279-4029		Sequence 4029, AP

ALIGNMENTS

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; Patent No. 6536962
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radivoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 78CIP2B
; CURRENT FILING NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_PLgenes Version 1.0
; SEQ ID NO 152
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398) ..(2329)
; QUERY Match 89.7%; Score 528.4; DB 3;
; Best Local Similarity 98.7%; Pred. No. 2,3e-146;
; Matches 543; Conservative 0; Mismatches 6;
; Indels 1; Gaps 1;

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Db 1118 GTTGTCCCTAAATGTTGCCAACAGTCATTGAGACTTAAGTCAGTCTTACTGATGACATGAG 120
 Qy 61 TCCATGTGCACCTAACAGAGATACTCAAGTCAGTCTTACTGATGACATGAG 1177
 Db 1178 TCCATGTGCACCTAACAGAGATACTCAAGTCATTGAGACTCATGGAG 1237
 Qy 121 GAACTAATTGAGACTTCAATTGATGCTCTGAGTCAAGAACGTTGCTGT 180
 Db 1238 GAACTAATTGAGACTTCAATTGATGCTCTGAGTCAAGAACGTTGCTGT 1297
 Qy 181 TTACCTAGGATGAAAACCTGACGCAAATGAGACTTCAAGTGATGAAAGCA 240
 Db 1298 TTACCTAGGATGAAAACCTGACGCAAATGAGACTTCAAGTGATGAAAGCA 1357
 Db 241 AATGTCGATCCCGTTGGGGCATGATTCCATGGTATTGCAACCCPTGCTAC 300
 Qy 1358 AATGTCGATCCCGTTGGGGCATGATTCCATGGTATTGCAACCCPTGCTAC 1417
 Qy 301 CGTCATATTCTTTAGATGAACTTATGATCCTTCTAGCTGAAGA 360
 Db 1418 CGTCATATTCTTTAGATGAACTTATGATCCTTCTAGCTGAAGA 1477
 Qy 361 AAGACCATGCCAACTACCTTAACTGAGAAGGGATAAACAGAAAAATAATTGAAATA 420
 Db 1478 AAGACCATGCCAACTACCTTAACTGAGAAGGGATAAACAGAAAAATAATTGAAATA 1537
 Qy 421 CCTTCAGAAAGAAATTCTAAAGTGTGCTGCTGCTGCTGCTGCTGCTAAACAT 480
 Db 1538 CCTTCAGAAAGAAATTCTAAAGTGTGCTGCTGCTGCTGCTGCTAAACAT 1597
 Qy 481 -TCACTGTAACGATTCGAAATCACAGGAAGGGGAACTAACAGCTGTGAC 539
 Db 1598 GTCACTGTAACGATTCGAAATCACAGGAAGGGGAACTAACAGCTGTGAC 1657
 Qy 540 TGATGACCAA 549
 Db 1658 CCTTCGGAA 1667

Db 380 GAACTAATTGAGCTT 396
 Qy 1 GTTGTCCCTAAATGATGTTGCCAACAGTCATTGAGACTCATGGAGCTCATGGAG 120
 Db 260 GTTGTCCCTAAATGATGTTGCCAACAGTCATTGAGACTCATGGAGCTCATGGAG 319
 Qy 61 TCCATGTGCACCTAACAGAGATACTCAAGTCAGTCTTACTGATGACATGAG 120
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 Qy 121 GAACTAATTGAGCTT 137

RESULT 3
 US-09-713-550-150
 ; Sequence 150, Application US/09713550
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; CURRENT APPLICATION NUMBER: US/09/713-550
 ; CURRENT FILING DATE: 2000-11-14
 ; NUMBER OF SEQ ID NOS: 205
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 150
 ; LENGTH: 396
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-713-550-150

Query Match 23.3%; Score 137; DB 3; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 380 GAACTAATTGAGCTT 396

Qy 1 GTTGTCCCTAAATGATGTTGCCAACAGTCATTGAGACTCATGGAGCTCATGGAG 120
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 Qy 61 TCCATGTGCACCTAACAGAGATACTCAAGTCAGTCTTACTGATGACATGAG 120
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 Qy 121 GAACTAATTGAGCTT 137

RESULT 4
 US-09-825-294-150
 ; Sequence 150, Application US/09825294
 ; Patent No. 6710170
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; CURRENT APPLICATION NUMBER: US/09/825-294
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 150
 ; LENGTH: 396
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-825-294-150

Query Match 23.3%; Score 137; DB 3; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 380 GAACTAATTGAGCTT 396

Qy 1 GTTGTCCCTAAATGATGTTGCCAACAGTCATTGAGACTCATGGAGCTCATGGAG 120
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ALIGNMENTS

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 361. AAGACCCTGCCAATCCTTAAAGAAGGGATAAACAGAAAATAATGTGAATA 420
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 481. TCACTGTAACCATTAACAGAGGGATAAACAGAAAATAATGTGAATA 420
 481. TCACTGTAACCATTAACAGAGGGATAAACAGAAAATAATGTGAATA 420
 541. GATGACCAAGGGAGCTGATGCCACAGATACTGCATIGAAATCTGG 589
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 Db 541 GATGACCAAGGGAGCTGATGCCACAGATACTGCATIGAAATCTGG 589
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 US-10-786-052-3
 ; Sequence 3, Application US/10786052
 ; Publication No. US20050113568A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHULWOOK, KIM
 ; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
 ; FILE REFERENCE: 3884-0115P
 ; CURRENT APPLICATION NUMBER: US/10/786,052
 ; CURRENT FILING DATE: 2004-02-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83652
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3
 ; LENGTH: 589
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire
 US-10-786-052-3
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 Best Local Similarity 100.0%; Pred. No. 7 6e-148;
 Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2778.314 Million cell updates/sec

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Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	41.2	7.0	2147	8 US-10-750-185-40169	Sequence 40169, A	
c	8	39.4	6.7	493	6 US-09-925-065A-301178	Sequence 301178,
c	9	39.4	6.7	493	6 US-09-925-065A-301179	Sequence 301179,
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c	12	37.8	6.4	2950	8 US-10-793-626-3349	Sequence 3349, AP
c	13	37.8	6.4	3378	12 US-11-136-527-2444	Sequence 2244, AP
c	14	37.8	6.4	3760	8 US-10-793-626-4029	Sequence 4029, AP
c	15	37.4	6.3	405	6 US-09-925-065A-406315	Sequence 406315,
c	16	37.4	6.3	577	6 US-09-925-065A-474125	Sequence 474125,
c	17	37.4	6.3	618	6 US-09-925-065A-494545	Sequence 94545,
c	18	37.4	6.3	643	6 US-09-925-065A-801427	Sequence 801427,
c	19	37.4	6.3	643	6 US-09-925-065A-801428	Sequence 801428,
c	20	37.4	6.3	643	6 US-09-925-065A-801429	Sequence 801429,

ALIGNMENTS

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US-09-925-065A-278866
; Sequence 278866, Application US/09925065A
; PUBLICATION NO. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 1038827..135
; CURRENT APPLICATION NUMBER: US/09-925-065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278866
Query Match 51.6%; Score 304; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1..2e-68;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTGTCCCTTAATATAATGTTGCCACCTACAGAGATACTTCAGTCTCTACTGAGTACATGAGATT 60
226 GTGTGTCCCTTAATATAATGTTGCCACCTACAGAGATACTTCAGTCTCTACTGAGTACATGAGATT 285
61 TCCAAATGTTGCCACCTACAGAGATACTTCAGTCTCTACTGAGTACATGAGATT 120
286 TCCAAATGTTGCCACCTACAGAGATACTTCAGTCTCTACTGAGTACATGAGATT 345
121 GAAGTAAATCAGGAGTCATTGATGTCAGTGTAGGAGTCAAGAACGTTCTGTCTGNT 180

Db	346	GAAGTAAATCAGGAGTTCAATTGATGCTGAGTCAGAAAGTGCTGTGTGT	405
Qy	181	TGACCTAGGGATGAAAACCTGACAGCAAATGAGTTGAAAAAGTGTGATAGGAAAGCA	240
Db	406	TGACCTAGGGATGAAAACCTGACAGCAAATGAGACTTGGAAAAGTGTGATAGGAAAGCA	465
Db	241	AATGTTGAAATCCTGTTCTGGGGCATGGTATTGCAACCCCTGTGAC	300
Qy	466	AATGTTGAAATCCTGTTCTGGGGCATGGTATTGCAACCCCTGTGAC	525
Qy	301	CGTC 304	
Db	526	CGTC 529	
RESULT 2			
US-09-925-065A-278867			
; Sequence 278867, Application US/09925065A			
; Publication No. US2004018104BA1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, David G.			
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome			
; FILE REFERENCE: 108827.135			
; CURRENT APPLICATION NUMBER: US/09/925,065A			
; CURRENT FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: US 60/243,096			
; PRIOR FILING DATE: 2000-10-24			
; PRIOR APPLICATION NUMBER: US 60/252,147			
; PRIOR FILING DATE: 2000-11-20			
; PRIOR APPLICATION NUMBER: US 60/250,092			
; PRIOR FILING DATE: 2000-11-30			
; PRIOR APPLICATION NUMBER: US 60/261,766			
; PRIOR FILING DATE: 2001-01-16			
; PRIOR APPLICATION NUMBER: US 60/289,846			
; PRIOR FILING DATE: 2001-05-09			
; NUMBER OF SEQ ID NOS: 957086			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO: 278867			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US-09-925-065A-278867			
Query Match 51.6%; Score 304; DB 6; Length 529;			
Best Local Similarity 100.0%; Pred. No. 1 2e-68; Mismatches 0; Indels 0; Gaps 0;			
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;			
Qy	1	GTTGTTCCCTTAATATGATGTTGCGAACGCTGATTCAGACTCTTACATGATGACATGAAAG	120
Db	226	GTTGTTCCCTTAATATGATGTTGCGAACGCTGATTCAGACTCTTACATGATGACATGAAAG	285
Qy	61	TCCATATGCCACCTACAGAGATACTTCAACTCTTACTGATGATCACATGAAAG	240
Db	286	TCCATATGCCACCTACAGAGATACTTCAACTCTTACTGATGATCACATGAAAG	345
Qy	121	GAAGTAAATCAGGAGTTCAATTGATGCTGAGTGAGCTCAAGAACCTGTCTGTGT	180
Db	346	GAAGTAAATCAGGAGTTCAATTGATGCTGAGTGAGCTCAAGAACCTGTCTGTGT	405
Qy	181	TGACCTAGGGATGAAAACCTGACAGCAAATGAACTTGTGATAGGAAAGCA	240
Db	406	TGACCTAGGGATGAAAACCTGACAGCAAATGAACTTGTGATAGGAAAGCA	465
Qy	241	AATGTTGCAATCCTGTTCTGGGGCATGGTATTGCAACCCCTGTGAC	300
Db	466	AATGTTGCAATCCTGTTCTGGGGCATGGTATTGCAACCCCTGTGAC	525
Qy	301	CGTC 304	
Db	526	CGTC 529	

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 2837,15 Seconds

Title: US-10-785-981-4

Perfect score: 469

Sequence: 1 catttataggggctacgcgc.....tagtgcattgaaatccctgg 469

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_dat: *
7: gb_ph: *
8: gb_pr: *
9: gb_o: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	408	2	87.0	1131	8 CR541796 Homo sapi	CR541796 Homo sapi AY893990 Synthetic
2	408	2	87.0	1134	11 AY893990	C0714735 Sequence CS119314 Sequence A8834441 Sequence
3	408	2	87.0	1374	6 C0714735	AK096902 Homo sapi
4	408	2	87.0	1374	6 CS119314	BC012597 Homo sapi CR536516 Homo sapi
5	408	2	87.0	1381	6 AX834441	CR536516 Human adult AB086240 Coryphaen
6	408	2	87.0	1381	8 AK096902	MJ12866 Mouse skele AB021652 Coryphaen
7	408	2	87.0	1694	8 BC012597	AB086242 Coryphaen BC014877 Mus muscu
8	406	6	86.7	1134	8 CR536516	AB021650 Coryphaen BC061974 Rattus no X03766 Mouse mRNA AB052654 Lampetra
9	406	6	86.7	1374	8 HUMACTASK	AB086240 Coryphaen
10	353	2	75.3	1587	5 AB086240	MUSACSM
11	352	2	75.1	1419	9 BC0161750	AB021652 Coryphaen
12	351	6	75.0	1568	5 AB086242	AB086242 Coryphaen
13	351	6	75.0	1582	5 AB086242	AB021650 Coryphaen
14	350	4	74.7	1457	9 C0714877	AB021650 Coryphaen
15	350	4	74.6	1611	5 AB021650	BC061974 Rattus no X03766 Mouse mRNA AB052654 Lampetra
16	348	8	74.4	1518	9 BC061974	AB021650 Coryphaen
17	347	2	74.0	1251	9 MMAXTASR	BC061974 Rattus no X03766 Mouse mRNA AB052654 Lampetra
18	347	2	74.0	2472	5 AB052654	AB052654 Lampetra

ALIGNMENTS

RESULT 1

CR541796 LOCUS Homo sapiens full open reading frame cDNA clone RZPD0834B061ID for gene ACTAI, actin, alpha 1, skeletal muscle; complete cds, without stopcodon.

CR541796 DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834B061ID for gene ACTAI, actin, alpha 1, skeletal muscle; complete cds, without stopcodon.

CR541796 ACCESSION CR541796.1 GI:49456548

VERSION Full ORF shuttle clone, Gateway(TM), complete cds.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1131)

AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDOR201)

JOURNAL Unpublished

COMMENT 2 (bases 1 to 1131)

AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

TITLE Direct Submission

JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

COMMENT RZPD; RZPD0834B0631D, ORFNO 3650

JOURNAL www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD LIB No. 834

COMMENT Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.

JOURNAL www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNO=834

COMMENT www.rzpd.de/cgi-bin/products/orfclones/

CONTACT Inge Arlaart

JOURNAL RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany

COMMENT Tel: +49 30 32639 100

CONTACT Fax: +49 30 32639 111

JOURNAL www.rzpd.de

This clone is available from RZPD.
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu: FUR130947.01L)
 This CDS clone is part of a collection of human full ORF clones
 Jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been cloned without stopcodon.
 The CDS has been inserted into pDONR201 via a BP Clonase (TM) reaction. Additional sequence has been added in front of the start codon: att_ATAAA GCA GGC TCC ACC (ATG). The last codon is followed by the 3' att site: GACCCAGCTTCTTCTT. . att The clone is validated by full sequence check.
 Compared to the reference sequence NM_001100 (GI:5016087) we did not find any amino acid exchanges.
 Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES

source

1. .1131
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="Human Full ORF Clones Gateway (TM) - RZPD"
 /clone_id="RZPD834B0631D"
 /comment="MCDDEDTALVCDCNGSGLUKAGAGDDAPRAVPSIYNGPRHQW
 VVGMGQDKDSYGEAQSQRGLILKYPERGLITNWDMCNIWHETFYNELRVABE
 HPTPLTEAPLNPKANREPMTOEMFTENPVPAVVAOAVLSYASERTTGIVLDSDG
 VTHNVPVIEGALPHAINRLDLAGDLTDYLMKLLTRGTSVTLAIBRIVDIREKL
 CYVALDFNEMATASSLESKEYLPQGVQTIGNERFRCPSTLFOPSFIMESAGI
 HETTYNSIMKCDIDIRKLYANNVMSGTTMPGIAADMROMKETALAPSTMKIKIAP
 PERKYSWIGGSILASLTFQQMWIIRQEYDAGPSIVHRCF"

ORIGIN

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 CATTATGAGGCTACCTGATGAAAGATCCTCATGTGGCTGAACTCTTC-TGACCACAC	87.0%	408.2	1131	97.9%	1.6e-58	0	0	1	1;
Db	498 CATTATGAGGCTACCTGATGAAAGATCCTCATGTGGCTGAACTCTTC-TGACCACAC									
Qy	61 TCTTACCGACTACCTGATGAAAGATCCTCATGTGGCTGAACTCTTC-TGACCACAC									
Db	558 TCTTACCGACTACCTGATGAAAGATCCTCATGTGGCTGAACTCTTC-TGACCACAC									
Qy	120 TGAGGGCAGATCTGGCGGACATCAAGGAGAACGCTGCTACGTGGCCCTGGACTTCCA									
Db	618 TGAGGGCAGATCTGGCGGACATCAAGGAGAACGCTGCTACGTGGCCCTGGACTTCCA									
Qy	180 GAACAGATGGGAAGCGCGCTCTCCCTGAAAGAGCTGAGCTGCCAGA									
Db	678 GAACAGATGGGAAGCGCGCTCTCCCTGAAAGAGCTGAGCTGCCAGA									
Qy	240 CGGGCAGGCTCATCACATCGGCAACGAGGCTTCCGGTCCCAGAACGCTCTTCAGCC									
Db	738 CGGGCAGGCTCATCACATCGGCAACGAGGCTTCCGGTCCCAGAACGCTCTTCAGCC									
Qy	300 CTCCCTCATCGGTATGGGAAGCGCGCTCTCCCTGAAAGAGCTGAGCTGCCAGA									
Db	798 CTCCCTCATCGGTATGGGAAGCGCGCTCTCCCTGAAAGAGCTGAGCTGCCAGA									
Qy	360 GTGTGACATCGACATCGGAGGACTGTATGCCAACAGCTATGTCCGGGGACCC									
Db	858 GTGTGACATCGACATCGGAGGACTGTATGCCAACAGCTATGTCCGGGGACCC									

Qy	420 TGATGACCAAGAG 432	LOCUS	AY893990	1134 bp mRNA linear	SYN 16-MAR-2005
Db	918 GATGTACCCGG 930	DEFINITION	(ACTA1) mRNA, partial cds.		
		ACCESSION	AY893990		
		VERSION	AY893990.1	GI:60832847	
		KEYWORDS	Human ORF Project.		
		SOURCE	synthetic construct		
		ORGANISM	synthetic construct		
			other sequences; artificial sequences.		
		REFERENCE	1 (bases 1 to 1134)		
		AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.		
		TITLE	Cloning of human full-length CDS FLEXGene in Gateway(TM) recombinational vector system		
		JOURNAL	Unpublished		
		REFERENCE	2 (bases 1 to 1134)		
		AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.		
		JOURNAL	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA		
		COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AtBEC recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence verified.		
		FEATURES	Location/Qualifier		
		source	1. .1134 /organism="synthetic construct" /mol_type="mRNA" /db_xref="taxon:32630" /clone="FLU130947.01L" /lab="Escherichia coli DH5alpha T1 resistant" /note="derived from Homo sapiens first strand cDNA library from Placenta and brain" 1. .>1134 /gene="ACTA1" /gene="ACTA1" /codon_start=1 /protein_id="CAG46595.1" /db_xref="GI:49465491" /translation="MCDEDTALVCDCNGSGLUKAGAGDDAPRAVPSIYNGPRHQW VVGMGQDKDSYGEAQSQRGLILKYPERGLITNWDMCNIWHETFYNELRVABE HPTPLTEAPLNPKANREPMTOEMFTENPVPAVVAOAVLSYASERTTGIVLDSDG VTHNVPVIEGALPHAINRLDLAGDLTDYLMKLLTRGTSVTLAIBRIVDIREKL CYVALDFNEMATASSLESKEYLPQGVQTIGNERFRCPSTLFOPSFIMESAGI HETTYNSIMKCDIDIRKLYANNVMSGTTMPGIAADMROMKETALAPSTMKIKIAP PERKYSWIGGSILASLTFQQMWIIRQEYDAGPSIVHRCF"		
			1. .>1134 /organism="synthetic construct" /mol_type="mRNA" /db_xref="taxon:32630" /clone="FLU130947.01L" /lab="Escherichia coli DH5alpha T1 resistant" /note="derived from Homo sapiens first strand cDNA library from Placenta and brain" 1. .>1134 /gene="ACTA1" /gene="ACTA1" /codon_start=1 /protein_id="AAK37027.1" /db_xref="GI:60832848" /translation="MCDEDTALVCDCNGSGLUKAGAGDDAPRAVPSIYNGPRHQW VVGMGQDKDSYGEAQSQRGLILKYPERGLITNWDMCNIWHETFYNELRVABE HPTPLTEAPLNPKANREPMTOEMFTENPVPAVVAOAVLSYASERTTGIVLDSDG VTHNVPVIEGALPHAINRLDLAGDLTDYLMKLLTRGTSVTLAIBRIVDIREKL CYVALDFNEMATASSLESKEYLPQGVQTIGNERFRCPSTLFOPSFIMESAGI HETTYNSIMKCDIDIRKLYANNVMSGTTMPGIAADMROMKETALAPSTMKIKIAP PERKYSWIGGSILASLTFQQMWIIRQEYDAGPSIVHRCF"		
			ORIGIN		
			Query Match	87.0%	Score 408.2; DB 11; Length 1134;
			Best Local Similarity	97.9%	Pred. No. 1.6e-58;
			Matches	424;	Conservative 0; Mismatches 8; Indels 1; Gaps 1;

20	308 .8	65 .8	1329	10	ADFe6557	Novel hum			
	21	308 .8	65 .8		Abl62474	Colon ade			
	22	308 .8	65 .8		Abl69196	Prostate			
	23	308 .8	65 .8		Abk35332	Gene ACTA			
	24	308 .8	65 .8		Adb70371	Vascular			
	25	308 .8	65 .8		Adm5551	Human BBC			
	26	308 .8	65 .8		Adj3150	Human mal			
	27	308 .8	65 .8		Acm39088	Tumour-as			
	28	308 .8	65 .8		Adz26568	Human smo			
	29	308 .8	65 .8		Acn90751	Breast ca			
	30	307 .4	65 .5		Aas61617	Jung smal			
	31	307 .2	65 .5		Ac15527	Human col			
	32	307 .2	65 .5		Acc44347	Gene enco			
	33	307 .2	65 .5		Abk35123	Human cDN			
	34	307 .2	65 .5		Adp03041	Human hou			
	35	307 .2	65 .5		Adbs8539	Human han			
	36	307 .2	65 .5		Adu0171	Housekeep			
	37	307 .2	65 .5		Ad162878	Human apo			
	38	307 .2	65 .5		Ad888823	Nucleotid			
	39	307 .2	65 .5		Ad888824	Nucleotid			
	40	307 .2	65 .5		Ad888822	Nucleotid			
	41	307 .2	65 .5		Abk84502	Human cDN			
	42	307 .2	65 .5		Ad226064	Human gen			
	43	307 .2	65 .5		Abv94253	Breast ca			
	44	307 .2	65 .5		Ad899314	Human act			
	45	307 .2	65 .5		Adp03061	Human hou			

ALIGNMENTS

RESULT 1
 geneseqn1990s;*
 geneseqn2000s;*
 geneseqn2001as;*
 geneseqn2001bs;*
 geneseqn2002as;*
 geneseqn2002bs;*
 geneseqn2003as;*
 geneseqn2003bs;*
 geneseqn2004cs;*
 geneseqn2004ds;*
 geneseqn2004as;*
 geneseqn2004bs;*
 geneseqn2005s;*
 ID AD289041
 standard; DNA; 469 BP.
 XX
 AC AD289041;
 XX
 DT 28-JUL-2005 (first entry)
 DE Pig growth factor I (GF IV) gene, seq id 4.
 XX
 KW Growth; biochip; swine; hog raising; growth factor IV; gene;
 XX
 OS Sus scrofa; Kagoshima Berkshire.

Required. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARY

Query										Result										
result	No.	Score			Match Length			DB ID			Description			PR	XX			XX		
		Query	Match	Length	DB	ID														
	1	469	100.0	469	14	ADZ89041									PA	(KIMC/)	KIM C.			
	2	469	100.0	469	14	ADZ79334									PA	(YEONJ/)	YEO J.			
	3	469	100.0	469	14	ADZ77171									PA	(LEEJ/)	LEE J.			
	4	408.2	87.0	1374	14	ADX25976									PA	(SONG Y.				
	5	408.2	87.0	1381	11	ADM02880									PA	(CHOK/)	CHO K.			
	6	359.5	76.5	461	8	ABx49264									PA	(CHUN/)	CHUNG K.			
	7	350.4	74.7	1446	14	ADZ60281									PA	(KIMI/)	KIM I.			
	8	347.2	74.0	1134	13	ADV41171									PA	(JIN/)	JIN S.			
	9	347.2	74.0	1134	14	ADX26223									PA	(PARK/)	PARK S.			
	10	347.2	74.0	1384	14	ADX25859									PA	(JUNG J.)	JUNG J.			
	11	325.2	69.3	1361	10	ADB53865									PA	(LEEM/)	LEE M.			
	12	325.2	69.3	1361	11	ADW22181									PA	(KWON/)	KWON E.			
	13	325.2	69.3	1780	14	ADZ60324									PA	(CHOE/)	CHO E.			
	14	312	66.5	1288	12	ADF45416									PA	(CHOH/)	CHO H.			
	15	312	66.5	1288	12	ADN03844									PA	(SHIN/)	SHIN S.			
	16	312	66.5	1288	13	ADR24777									PA	(NAMH/)	NAM H.			
	17	312	66.5	1288	14	ADY54924									PA	(HONG G/)	HONG Y.			
c	18	312	66.5	1404	4	AAR72871									PA	(HONG G/)	HONG S.			
	19	308.8	65.8	1275	2	AAT72871									PA	(KANG Y.)	KANG Y.			
															PA	(HA Y.)	HA Y.			

PA	(ROUJ/)	ROU J.	ID	ADZ79334 standard; cDNA; 469 BP.
PA	(KWAC/)	KWACK S.	XX	
PA	(CHOI/)	CHOI I.	AC	
PA	(KIMB/)	KIM B.	XX	
XX	Kim C,	Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;	XX	28-JUL-2005 (first entry)
PI	Park S,	Jung J, Lee M, Kwon E, Cho B, Shin S, Nam H;	XX	Swine growth factor GF-IV cDNA for cDNA chip diagnostic method.
PI	Hong Y,	Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;	XX	
XX	DR	WPI: 2005-403240/41.	XX	
PT	Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.	XX	XX	
PT	Claim 2; SEQ ID NO 4; spp; English.	XX	XX	
XX	The invention relates to a functional cDNA chip (I) for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises a probe comprising growth specific genes in muscle and fat tissues of swine, and a substrate on which the probe is immobilized. Further disclosed is a kit (K1) useful for screening and functional analysis of growth specific gene according to breeds and tissues of swine, comprising (I) integrated in it, Cys-dCTP or Cy3-dCTP bound cDNA from RNA of the tissue to be screened, a fluorescence scanning system, and a computer analysis system (II) and (K1) are useful for screening and function analysis of growth specific gene according to breeds and tissues of swine. (I) is useful in the swine improvement and breeding of a new breed, and in the hog raising industry. The current sequence represents the pig growth factor IV (GF IV) gene.	XX	XX	
XX	Sequence 469 BP; 106 A; 146 C; 133 G; 84 T; 0 U; 0 Other;	XX	XX	
SQ	Query Match 100.0%; Score 469; DB 14; Length 469;	XX	XX	
	Best Local Similarity 100.0%; Pred. No. 1-4e-100;	XX	XX	
	Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	
Qy	1 CATTATGAGGGCTACGGCTACGCCATATGCCCTGGACCATCTGGCGAGCGCGCA 60	XX	XX	
Db	1 CATTATGAGGGCTACGGCTACGCCATATGCCCTGGACCATCTGGCGAGCGCGCA 60	XX	XX	
Qy	61 TCTTACCGACTACCTGATGAGATCTCATGAGATCTCATGAGGTGCTACTCTTGACCACAGT 120	XX	XX	
Db	61 TCTTACCGACTACCTGATGAGATCTCATGAGATCTCATGAGGTGCTACTCTTGACCACAGT 120	XX	XX	
Qy	121 GAGCGGAATGATGTTGGGAGCATCAGGAGAGCTGGCTGAGCTGGCTGGAG 180	XX	XX	
Db	121 GAGCGGAATGATGTTGGGAGCATCAGGAGAGCTGGCTGAGCTGGCTGGAG 180	XX	XX	
Qy	181 AACGAGATGGGAGACGCCGCTCCCTCTCCCTGGAAAGAGGTACAGAGTCAGAC 240	XX	XX	
Db	181 AACGAGATGGGAGACGCCGCTCCCTCTCCCTGGAAAGAGGTACAGAGTCAGAC 240	XX	XX	
Qy	241 GGGCAAGTCAATCACATGGAAAGGGGCTTCGGTGCCTGGCGGAGACGCTCTTCAGCCC 300	XX	XX	
Db	241 GGGCAAGTCAATCACATGGAAAGGGGCTTCGGTGCCTGGCGGAGACGCTCTTCAGCCC 300	XX	XX	
Qy	301 TCCTTCATCGGTATGGAGTGGCTGGGGCATTCAGAACCTAACCCCTGCTGGGGACCCAGT 360	XX	XX	
Db	301 TCCTTCATCGGTATGGAGTGGCTGGGGCATTCAGAACCTAACCCCTGCTGGGGACCCAGT 360	XX	XX	
Qy	361 TGTGACATGGACATCAGGAAGGACCTGTAATGCCAACCCCTGCTGGGGACCCAGT 420	XX	XX	
Db	361 TGTGACATGGACATCAGGAAGGACCTGTAATGCCAACCCCTGCTGGGGACCCAGT 420	XX	XX	
Qy	421 GATGACCAAGGAGGTGATGGCCACAGATGTGCCATGAAATCTGG 469	XX	XX	
Db	421 GATGACCAAGGAGGTGATGGCCACAGATGTGCCATGAAATCTGG 469	XX	XX	
PS	Claim 9; SEQ ID NO 4; 15pp; English.	XX	XX	
CC	The invention relates to a cDNA chip for screening and function analysis of swine genes comprising a probe capable of detecting marker genes specifically expressed in the muscle and fat tissues of swine and a substrate on which the probe is immobilized. The invention also includes a kit for screening and function analysis of swine genes comprising the cDNA chip. The cDNA chip is useful for comparing genetic expression according to swine genes, particularly for comparing genetic mutation screening, genetic polymorphism interpretation, development of new drugs for disease treatment and disease diagnosis, swine improvement. This sequence corresponds to the cDNA for a growth factor detected using the chip of the invention.	CC	CC	
SQ	Sequence 469 BP; 106 A; 146 C; 133 G; 84 T; 0 U; 0 Other;	XX	XX	

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 2778.76 Seconds
 (without alignments)

Title: US-10-785-981-4
 Perfect score: 469
 Sequence: 1 cattatagggttacgcgc.....tagtgcattgaaatccctgg 469

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_htc:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_gbss1:
 10: gb_gbss2:
 11: gb_gbss3:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
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2	408.2	87.0	524	2	BF769879	RC3-IT001	BP11694 BP31694
3	408.2	87.0	583	3	BP31694	CR552285 AGENCOURT	DR174141 HR0001
4	408.2	87.0	872	6	BP826015	MR2-HN003	BK199822 DK72p779J
5	408	87.0	520	8	DR174141		BP219712 BP319712
6	406.6	86.7	576	5	BK499822		CR791305 DK72p468B
7	402.4	86.3	598	3	BP317419		CB483530 EST_038 S
8	403.4	86.0	615	4	BP769879		CD610657 56089031H
9	403.4	86.0	583	7	CN363604		BP219352 BP19352
10	403.4	86.0	1543	4	CR859327		BP265037 BP65037
c 11	403.2	86.0	527	3	BP826015		AU710329 BF790986 602251034
c 12	403.2	86.0	581	3	BP319712		AA180732 zp43d03 X
c 13	402.4	85.8	765	6	CR72996		DN413152 Lib4215-0
c 14	401	85.5	519	6	CB483530		BP265026 BP265026
c 15	400.2	85.3	686	6	CD610657		
c 16	399	85.1	583	3	BP319352		
c 17	392.2	83.6	628	3	BP265037		
c 18	391.2	83.4	532	1	AJ710329		
c 19	385.2	82.9	827	2	BF790986		
c 20	384.2	81.9	585	1	AA180732		
c 21	381.8	81.4	634	8	DN413152		
c 22	381	81.2	526	3	BP265026		

ALIGNMENTS

RESULT 1

BF826972

LOCUS

RC1-HN0031-221100-012-h12

mRNA

linear

HN0031

Homo sapiens

cDNA

mRNA

sequence

EST

BF826972.1

GI:12170455

VERSION

EST.

Homo sapiens

(human)

ORGANISM

Eukaryota

Metazoa

Chordata

Craniata

Vertebrata

Bureostomi

Mammalia

Butheria

Buarchontoglires

Primates

Catarrhini

Hominoidea

Homino

REFERENCE

1 (bases 1 to 483)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baiu,G.S., Simpson,D.H., Brunet,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., Simpson,A.J.

TITLE

shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

PUBLISHED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: aaimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-HN0031-221100-012-h12&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 483.

Location/Qualifiers

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/mol_type="mRNA"

/db_xref="Taxon:9606"

/dev_stage="Adult"

/clone_id="HN0031"

/note="Organ: head_normal; Vector: puci8; Site_1: SmaI;

Site 2: SmalI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.¹

ORIGIN

Query Match 87.0%; Score 408.2; DB 2; Length 483;
Best Local Similarity 97.9%; Pred. No. 1.2e-89;
Matches 424; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy	Db	FEATURES source	ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
Qy	1	CATTATGAGGTCTGGCTGCCACGCCATATGGCCTGACCCGCGCA 60		87.0%	97.9%	408.2	DB 2	Length 524;
Db	51	CATTATGAGGTCTGGCTGCCACGCCATATGGCCTGACCCGCGCA 110		97.9%	97.9%	408.2	Pred. No. 1.2e-89;	
Qy	61	TCTTACCGGACTACCTGATGAAATCCTCACTGAGCTGCTACTCTTC-TGACCAAC 119		97.9%	97.9%	408.2	Matches 424;	
Db	111	TCTTACCGGACTACCTGATGAAATCCTCACTGAGCTGCTACTCTTC-TGACCAAC 170		97.9%	97.9%	408.2	Conservative 0;	
Qy	120	TGAGCCGCAGATCGGCCGACATCAGAGAAGCTGTTACCTGGCCCTGACTTCGA 179		97.9%	97.9%	408.2	Mismatches 8;	
Db	171	TGAGCCGCAGATCGGCCGACATCAGAGAAGCTGTTACCTGGCCCTGACTTCGA 230		97.9%	97.9%	408.2	Indels 1;	
Qy	180	GAACAGATGGCACGGCCCTCTCCCTGGAAAAGGCTAGAGTCGCCAGA 239		97.9%	97.9%	408.2	Gaps 1;	
Db	231	GAACAGATGGCACGGCCCTCTCCCTGGAAAAGGCTAGAGTCGCCAGA 290		97.9%	97.9%	408.2	Location/Qualifiers	
Qy	240	CGGGCGGGTCATCACCATTGGCAACGGGGCTTCCGGTCCCAGAACCTAACAGCTCATGAA 299		97.9%	97.9%	408.2	1. 524	
Db	291	CGGGCGGGTCATCACCATTGGCAACGGGGCTTCCGGTCCCAGAACCTAACAGCTCATGAA 350		97.9%	97.9%	408.2	/organism="Homo sapiens"	
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Db	351	CTCCCTCATCGGTATGGATGGCTGGGGGAAATTCAAGAACCCATACAAAGCTCATGAA 410		97.9%	97.9%	408.2	/db_xref="Taxon:9606"	
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Db	471	GATGACCTCTGG 483		97.9%	97.9%	408.2	No. 1.2e-89;	
RESULT 2	BF769879	BF769879_524 bp mRNA linear EST 12-JAN-2001		97.9%	97.9%	408.2	Indels 1;	
LOCUS	RC3-ITR0011-161100-022-a03	RC3-ITR0011 Homo sapiens CDNA, mRNA sequence.		97.9%	97.9%	408.2	Gaps 1;	
DEFINITION				97.9%	97.9%	408.2	Location/Qualifiers	
ACCESSION	BF769879	GI:12117779		97.9%	97.9%	408.2	1. 524	
VERSION	EST.			97.9%	97.9%	408.2	/organism="Homo sapiens"	
KEYWORDS				97.9%	97.9%	408.2	/note="Organism: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 524)	
SOURCE	Homo sapiens (human)			97.9%	97.9%	408.2		
ORGANISM				97.9%	97.9%	408.2		
REFERENCE	Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, S.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., Ohare, M.J., Soares, F., Brantani, R.R., Reis, L.P., de Souza, S.J., and Simpson, A.J.			97.9%	97.9%	408.2	Comments	
AUTHORS				97.9%	97.9%	408.2	Sequence tags	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			97.9%	97.9%	408.2	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
PUBMED	10737800			97.9%	97.9%	408.2	Comments	
TITLE				97.9%	97.9%	408.2	Comments	
COMMENT	Contact: Simpson, A.J.-G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, Brazil			97.9%	97.9%	408.2	Comments	
LOCATION	BP316694	BP316694 Sugano cDNA library, pericardium Homo sapiens cDNA clone		97.9%	97.9%	408.2	Comments	
DEFINITION	PCD02015,	PCD02015, mRNA sequence.		97.9%	97.9%	408.2	Comments	
ACCESSION	BP316694.1	BP316694.1 GI:52245669		97.9%	97.9%	408.2	Comments	
VERSION	EST.			97.9%	97.9%	408.2	Comments	
KEYWORDS				97.9%	97.9%	408.2	Comments	
SOURCE	Homo sapiens (human)			97.9%	97.9%	408.2	Comments	
ORGANISM	Homo sapiens			97.9%	97.9%	408.2	Comments	

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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC3&t2=RC3-ITR0011-161100-022-a03&t3=2000-11-16&t4=1>)

Seq primer: puc 18 forward

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High quality sequence stop: 524.

Location/Qualifiers

1. 524

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="Taxon:9606"

/dev_stage="Adult"

/clone_lib="ITR001"

/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="Taxon:9606"

/dev_stage="Adult"

/clone_lib="ITR001"

/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

1. 524

/organism="Homo sapiens"

/mol type="mRNA"

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/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

1. 524

/organism="Homo sapiens"

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Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/organism="Homo sapiens"

/mol type="mRNA"

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/clone_lib="ITR001"

/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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High quality sequence start: 12

High quality sequence stop: 524.

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Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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High quality sequence start: 12

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Location/Qualifiers

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/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/mol type="mRNA"

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/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

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High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="Taxon:9606"

/dev_stage="Adult"

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/note="Organ: epid rumor; Vector: puc18; Site: 1: SmalI;

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Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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/organism="Homo sapiens"

/mol type="mRNA"

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/dev_stage="Adult"

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Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 524.

Location/Qualifiers

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Site: 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Seq primer: puc 18 forward

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OM nucleic - nucleic search, using sw model.

Run on: February 20, 2006, 11:15:29 ; Search time 115,079 Seconds

(without alignments) 7244,353 Million cell updates/sec

Title: US-10-785-981-4
Perfect score: 469
Sequence: 1 catttatggatcgctacgccc.....tagccattgtaaatccctgg 469

Scoring table: IDENTITY NUC
GapOp 10.0 , GapExt 1.0

Searched: 1303057 seqs, 880780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: /cn2_6/pododata/1/ina1_backfile.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	312	66.5	1288	3 US-09-949-016-229	Sequence 229, APP Sequence 4886, APP
2	312	66.5	1288	3 US-09-949-016-4886	Sequence 1850, APP Sequence 2, APP
3	308.8	65.8	1275	2 US-08-588-113-1	Sequence 3553, APP Sequence 496, APP Sequence 345, APP
4	308.8	65.8	1312	3 US-09-949-016-1850	Sequence 15, APP Sequence 1, APP
5	308.8	65.8	1330	3 US-09-917-254-2	Sequence 32, APP
6	307.2	65.5	1919	3 US-09-949-016-3553	Sequence 730, APP
7	307.2	65.5	2376	3 US-09-976-594-496	Sequence 887, APP
8	307.2	65.5	4143	3 US-09-919-039-445	Sequence 5442, APP
9	305.6	65.2	1100	3 US-09-949-016-4538	Sequence 373, APP
10	305.6	65.2	1128	3 US-09-106-217-15	Sequence 1, APP
11	305.6	65.2	1134	3 US-09-106-217-1	Sequence 15, APP
12	304	64.8	1393	3 US-09-919-172-12	Sequence 4, APP
13	294.4	62.8	1489	3 US-09-976-594-730	Sequence 4, APP
14	294.4	62.8	1793	3 US-10-131-827-730	Sequence 4, APP
15	294.4	62.8	1814	3 US-09-949-016-4442	Sequence 373, APP
16	284.8	62.8	3128	3 US-09-191-039-373	Sequence 1, APP
17	284.8	60.7	1131	3 US-09-137-130-1	Sequence 1, APP
18	257.6	54.9	183770	3 US-09-949-016-15494	Sequence 15, APP
19	253.2	54.0	3240	3 US-09-171-337-14	Sequence 4, APP
20	253.2	54.0	3240	3 US-09-631-022-4	Sequence 4, APP
21	250	53.3	3748	2 US-08-261-206A-76	Sequence 76, APP
22	249	53.1	5643	2 US-08-144-602B-4	Sequence 4, APP
23	243.2	51.9	1481	3 US-09-533-559-7	Sequence 7, APP
24	238.8	50.9	2994	3 US-09-171-337A-3	GENERAL INFORMATION

RESULTS

RESULT 1

US-09-949-016-229 ; Sequence 229, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: CL001307
; CURRENT APPLICATION NUMBER: US/09-949-016-11971
; PRIORITY APPLICATION NUMBER: 2000-04-14
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 229
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-229

Query Match 66.5% ; Score 312, DB 3, Length 1288;
Best Local Similarity 85.5%; Pred: No 1, 3e-68;
Matches 359; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09-949-016-11971
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 229
LENGTH: 1288
TYPE: DNA
ORGANISM: Human
US-09-949-016-229

ALIGNMENTS

Db 815 TGGGAGGTATCCATTGCAATGAGGCCCTGGCTAGACCTCTTCAGGC 874
 Qy 300 CTCCCTCATGGTATGGATGGTGGCGGATTCAAGAGACCTAACAGCATGAA 359
 Db 875 TTCCCTTATGGCATGGATGGCTGGGAATTCAAGAACCTAACATCCATGAA 934
 Qy 360 GTGTGACATGGACATGGAGGAGCTGTATGTCGGGCCACCA 419
 Db 935 GTGTSACATGGACATGGAGGAGCTGTATGTCGGGCCACCA 994

RESULT 2
 US-09-949-016-4886
 Sequence 4886 Application US/0949016
 Patent No. 6912319

GENERAL INFORMATION:
 APPLICANT: McHugh, Kirk M.
 TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ADDRESS: No. 5710003ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/588,113
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
 NAME: Ralph, Rebecca L.
 REGISTRATION NUMBER: 35,152
 REFERENCE/DOCKET NUMBER: TUU-1652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1275 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 55..1186
 US-08/588-113-1

Query Match 66.5%; Score 312; DB 3; Length 1288;
 Best Local Similarity 85.5%; Pred. No. 1.3e-68;
 Matches 359; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

Db 575 TCTTACCGACTACCTGATGAGATCCTACTGAGGGTGTGTTACCTCC-TTCTGACCACAC 119
 Qy 1 CATTATGAGGTACGGCTGCGCCACGCATATGGCTGACCTGGCTGGCCATATGGCCATATGGCTGCGCCAC 60
 Db 635 CCTCAGGACTACCTCATGAGATCCTACAGAGGGTATTCTTGTGACACAC 694
 Qy 61 TCTTACCGACTACCTGATGAGATCCTACTGAGGGTGTGTTACCTGGCCCTGGACTTC 179
 Db 120 TGAGGCCGAGATCGGGCGCACATCAAGGAGAACGTGTGTTACCTGGCCCTGGACTTC 179
 Qy 695 TGAGGAGAATTGSGAGACATCAAGGAGAACGTGTGTTATGGCCCTGGACTTC 754
 Db 180 GAACGAGATGGCAEGCGCCTCCCTCTCCCTGAAAAGAGCTAAGGTGCCAGA 239
 Qy 755 GAATGAGATGGCAAGGAGCTAAGGTGCCAGA 814
 Db 240 CGGGAGGTATGGCTGGGGGAACTTCAAGAACCTAACAGGACATGAA 299
 Qy 815 TGGGAGGTATCACATTGCAATGAGGGCTTCAGCC 874
 Db 300 CTCCCTCATGGTATGGATGGGGGGGAACTTCAAGAACCTAACAGGACATGAA 359
 Qy 875 TTCCCTTATGGCATGGATGGGGGGGAACTTCAAGAACCTAACAGGACATGAA 934
 Db 360 GTGTGACATGGACATGGAGGACCTGTATGGCAAAAGCTCATGTCGGGGACAC 419
 Qy 935 GTGTGACATGGACATGGAGGACTATGGCTCTCTGGGGACAC 994
 Db 360 GTGTGACATGGACATGGAGGACCTGTATGGCAAAAGCTCATGTCGGGGACAC 419
 Qy 909 GTGTGACATGGACATGGAGGACTATGGCTCTCTGGGGACAC 968
 Db 909 GTGTGACATGGACATGGAGGACTATGGCTCTCTGGGGACAC 908

RESULT 3
 Sequence 1, Application US/08588113
 Patent No. 5710003

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 567.737 Seconds
(without alignments)

6831.225 Million cell updates/sec

Title: US-10-785-981-4

Perfect score: 469

Sequence: 1 catttataggggctacgcgc.....tagtggccatgttaaatcctgg 469

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

RESULT 1
US-10-785-981-4

; Sequence 4, Application US/10785981
; Publication No. US20050112597A1
; GENERAL INFORMATION:
; APPLICANT: CHULWOOK, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
; FILE REFERENCE: 3884-0120P
; CURRENT APPLICATION NUMBER: US/10/785,981
; CURRENT FILING DATE: 2004-06-26
; PRIORITY APPLICATION NUMBER: KR 2003-836553
; PRIORITY FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire

US-10-785-981-4

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
2	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
3	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
4	405.2	87.0	1381	6	US-10-108-260A-1565		Sequence 1565, AP
5	406.6	86.7	1374	7	US-10-124-425-1260		Sequence 1260, AP
6	359.9	76.5	461	3	US-09-960-352-14429		Sequence 14429, A
7	350.4	74.7	1446	9	US-10-764-120-5		Sequence 5, Appli
8	347.2	74.0	1134	7	US-10-191-803-116		Sequence 116, APP
9	325.2	69.3	1361	6	US-10-388-934-560		Sequence 560, APP
10	322.2	69.3	1780	9	US-10-764-120-48		Sequence 48, Appli
11	312	66.5	1288	6	US-10-341-434-100		Sequence 100, APP
12	312	66.5	1288	6	US-10-172-118-638		Sequence 638, APP
13	312	66.5	1288	9	US-10-342-887-638		Sequence 638, APP
14	312	66.5	1288	9	US-10-923-035-17		Sequence 17, Appli
15	308.8	65.8	1330	3	US-09-969-708-62		Sequence 62, Appli
16	308.8	65.8	1330	3	US-09-873-367-C-811		Sequence 811, Appli
17	308.8	65.8	1330	6	US-10-236-031B-63		Sequence 63, Appli
18	308.8	65.8	1330	8	US-10-370-715B-231		Sequence 231, Appli
19	308.8	65.8	1330	9	US-10-843-641A-811		Sequence 811, Appli
20	308.8	65.8	1330	9	US-10-843-641A-7533		Sequence 7533, AP
21	308.8	65.8	1948	5	US-10-198-846-11901		Sequence 11901, A
22	307.4	65.5	501	3	US-09-833-790-158		Sequence 158, APP
23	307.2	65.5	1400	9	US-10-956-157-5886		Sequence 5886, AP

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
2	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
3	469	100.0	469	9	US-10-785-981-4		Sequence 4, Appli
4	405.2	87.0	1381	6	US-10-108-260A-1565		Sequence 1565, AP
5	406.6	86.7	1374	7	US-10-124-425-1260		Sequence 1260, AP
6	359.9	76.5	461	3	US-09-960-352-14429		Sequence 14429, A
7	350.4	74.7	1446	9	US-10-764-120-5		Sequence 5, Appli
8	347.2	74.0	1134	7	US-10-191-803-116		Sequence 116, APP
9	325.2	69.3	1361	6	US-10-388-934-560		Sequence 560, APP
10	322.2	69.3	1780	9	US-10-764-120-48		Sequence 48, Appli
11	312	66.5	1288	6	US-10-341-434-100		Sequence 100, APP
12	312	66.5	1288	6	US-10-172-118-638		Sequence 638, APP
13	312	66.5	1288	9	US-10-342-887-638		Sequence 638, APP
14	312	66.5	1288	9	US-10-923-035-17		Sequence 17, Appli
15	308.8	65.8	1330	3	US-09-969-708-62		Sequence 62, Appli
16	308.8	65.8	1330	3	US-09-873-367-C-811		Sequence 811, Appli
17	308.8	65.8	1330	6	US-10-236-031B-63		Sequence 63, Appli
18	308.8	65.8	1330	8	US-10-370-715B-231		Sequence 231, Appli
19	308.8	65.8	1330	9	US-10-843-641A-811		Sequence 811, Appli
20	308.8	65.8	1330	9	US-10-843-641A-7533		Sequence 7533, AP
21	308.8	65.8	1948	5	US-10-198-846-11901		Sequence 11901, A
22	307.4	65.5	501	3	US-09-833-790-158		Sequence 158, APP
23	307.2	65.5	1400	9	US-10-956-157-5886		Sequence 5886, AP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 2
 US-10-789-723-4
 ; Sequence 4, Application US/10789723
 ; Publication No. US20050112602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHULWOOK, KIM
 ; TITLE OF INVENTION: CDNA CHIP FOR SCREENING SPECIFIC GENES AND ANALYZING THEIR
 ; FILE REFERENCE: YL0P040109US
 ; CURRENT APPLICATION NUMBER: US/10/789,723
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIORITY APPLICATION NUMBER: KR 2003-83651
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO: 4
 ; LENGTH: 469
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire
 ;
 US-10-789-723-4
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 Best Local Similarity 100.0%; Pred. No. 2e-128;
 Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 TCTCACCGACTACCTGATGAAGATCTRACTGCGTGCCTACTCTGACCA 120
 Qy 1 GAGGGAGATCCGGGACATCAAGGAAAGCTGTGCTACCTGGCCCTGGACTTCGAG 180
 Db 1 GAGGGAGATCCGGGACATCAAGGAAAGCTGTGCTACCTGGCCCTGGACTTCGAG 180
 Qy 1 AACAGATGGGAGGCCCTCTGGAAAAGAGCTAGAGCTGTTGCTACTGGCC 240
 Db 1 AACAGATGGGAGGCCCTCTGGAAAAGAGCTAGAGCTGTTGCTACTGGCC 240
 Qy 1 CATTATGAGGGTACCTGATGAAGATCTCTGACCA 60
 Db 1 CATTATGAGGGTACCTGATGAAGATCTCTGACCA 60
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 Db 1 TCTCACCGACTACCTGATGAAGATCTCTGACCA 120
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 Db 1 AACAGATGGCGACATCAAGGAAAGCTGTGCTACCTGGCCCTGGACTTCGAG 240
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 Db 1 GGGCAAGTCCATGAGGCTTCCCTCCCTGGAAAGAGCTACAGGCTCCAGC 300
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 Db 1 TCTCACCGACTACCTGATGAAGATCTCTGACCA 360
 Qy 1 TGTGACATGGACATGGAGGACTGCGACATGGCTACGGTGGCTACTCTGACCA 420
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 Db 1 GATGACCAAGGAGCTGATGCCACAGATAGTCATGGCAATCTGG 469
 Qy 1 GATGACCAAGGAGCTGATGCCACAGATAGTCATGGCAATCTGG 469
 Db 1 GATGACCAAGGAGCTGATGCCACAGATAGTCATGGCAATCTGG 469
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 RESULT 4
 US-10-789-723-4
 ; Sequence 4, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5438
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1565
 ; LENGTH: 1.381
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ;
 RESULT 3

RESULT 2

DROSOPH/C DROSOPH LOCUS Drosophila melanogaster DEFINITION Drosophila melanogaster serendipity (sry h-1) gene, complete cds. ACCESSION M23391 VERSION M23391.1 GI:340903 SOURCE DNA-binding protein; multifingered protein gene. ORGANISM Drosophila melanogaster

Bukaryota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.

REFERENCE 1. (bases to 4001)

AUTHORS Vincent, A., Kejzarkova-Lepesant,J., Segalat,L., Yanicosaras,C. and Lepesant,J.A.

TITLE sry h-1, a new Drosophila melanogaster multifingered protein gene showing maternal and zygotic expression

JOURNAL Mol. Cell. Biol. 8 (10), 4459-4468 (1988)

PUBLMED Original source text: Drosophila melanogaster (strain Canton S) (library: Lauer and Maniatis) DNA.

FEATURES Location/Qualifiers 1..4001

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="Canton S"

/db_xref="taxon:7227"

/map="region 98EF"

/tissue_libr="Lauer and Maniatis"

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/gene="sry h-1"

mRNA /join(399..1661,1722..2926,3037..3751)

/note="mRNA including exon 1a"

exon 399..1661

/gene="sry h-1"

/note="version a of exon 1"

/number=1

/join(410..1661,1722..2926,3037..3751)

/gene="sry h-1"

/note="mRNA including exon 1b"

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/gene="sry h-1"

/note="version b of exon 1"

/number=1

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/gene="sry h-1"

/note="mRNA including exon 1c"

exon 419..1661

/gene="sry h-1"

/note="version c of exon 1"

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/gene="sry h-1"

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/codon_start=1

CDS /product="DNA-binding protein"

/protein_id="AAA28487_1"

/db_xref="GI:387593"

/translation="MEGGKGEGRKMKKEAPSKKLPPKTYGGIDAGTPTKAHHDEBILSSL

RESULT 2

DROSOPH/C DROSOPH LOCUS Drosophila melanogaster DEFINITION Drosophila melanogaster serendipity (sry h-1) gene, complete cds. ACCESSION M23391 VERSION M23391.1 GI:340903 SOURCE DNA-binding protein; multifingered protein gene. ORGANISM Drosophila melanogaster

Bukaryota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.

REFERENCE 1. (bases to 4001)

AUTHORS Vincent, A., Kejzarkova-Lepesant,J., Segalat,L., Yanicosaras,C. and Lepesant,J.A.

TITLE sry h-1, a new Drosophila melanogaster multifingered protein gene showing maternal and zygotic expression

JOURNAL Mol. Cell. Biol. 8 (10), 4459-4468 (1988)

PUBLMED Original source text: Drosophila melanogaster (strain Canton S) (library: Lauer and Maniatis) DNA.

FEATURES Location/Qualifiers 1..4001

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="Canton S"

/db_xref="taxon:7227"

/map="region 98EF"

/tissue_libr="Lauer and Maniatis"

gene /join(399..1661,1722..2926,3037..3751)

/gene="sry h-1"

mRNA /join(399..1661,1722..2926,3037..3751)

/note="mRNA including exon 1a"

exon 399..1661

/gene="sry h-1"

/note="version a of exon 1"

/number=1

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/gene="sry h-1"

/note="mRNA including exon 1b"

exon 410..1661

/gene="sry h-1"

/note="version b of exon 1"

/number=1

/join(419..1661,1722..2926,3037..3751)

/gene="sry h-1"

/note="mRNA including exon 1c"

exon 419..1661

/gene="sry h-1"

/note="version c of exon 1"

/number=3

/join(649..1661,1722..2926,3037..3425)

/gene="sry h-1"

/standard_name="serendipity"

/codon_start=1

CDS /product="DNA-binding protein"

/protein_id="AAA28487_1"

/db_xref="GI:387593"

/translation="MEGGKGEGRKMKKEAPSKKLPPKTYGGIDAGTPTKAHHDEBILSSL

RESULT 3

CP000095_06

WCOMMENT

Sequence split into 19 fragments LOCUS CP000095 Accession CP000095

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CP000095_12		200001	310000
CP000095_03		300001	410000
CP000095_04		400001	510000
CP000095_15		500001	610000
CP000095_06		600001	710000
CP000095_07		700001	810000
CP000095_18		800001	910000
CP000095_09		900001	1010000
CP000095_10		1000001	1110000
CP000095_11		1100001	1210000
CP000095_12		1200001	1310000
CP000095_13		1300001	1410000
CP000095_14		1400001	1510000
CP000095_15		1500001	1610000
CP000095_16		1600001	1710000
CP000095_17		1700001	1810000
CP000095_18		1800001	1842899

Continuation (7 of 19) of CP000095 from base 600001 (CP000095 Prochlorococcus marinus st

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 430.26 Seconds
 (without alignments)
 7853.391 Million cell updates/sec

Title: US-10-785-981-5
 Perfect score: 507
 Sequence: 1 tataatagaaccgaaatcacgt.....tctgtcggtttcagccggag 507

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3312346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :	N_Genesegn_21:*
	1: genesegn1980s;*
	2: genesegn1990s;*
	3: genesegn2000s;*
	4: genesegn2001as;*
	5: genesegn2001bs;*
	6: genesegn2002as;*
	7: genesegn2002bs;*
	8: genesegn2003as;*
	9: genesegn2003bs;*
	10: genesegn2003cs;*
	11: genesegn2003ds;*
	12: genesegn2004as;*
	13: genesegn2004bs;*
	14: genesegn2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	507	100.0	507	14 AD289042	Adz89042 Pig growth factor I (GF V) gene, seq id 5.	
2	507	100.0	507	14 AD279335	Adz79335 Swine growth factor I (GF V) gene, seq id 5.	
3	507	100.0	507	14 AD277172	Adz77172 Pig growth factor I (GF V) gene, seq id 5.	
C 4	42.4	8.4	2000	8 ADA1938	Aaz00010 Rice Gene	
C 5	41.4	8.2	336	2 AAZ00010	Aax88092 Synthetic	
C 6	41.4	8.2	336	2 AAZ00010	Acl130038 Rice abiotic stress response protein	
C 7	40.8	8.0	891	11 ACI130038	Aax88093 Synthetic	
JIN S.	8	39.8	7.9	336	2 AAXX8093	Abl02625 Drosophila
C 9	39.8	7.9	2852	4 ABL02625	Abk92192 Prostate	
C 10	39.8	7.9	5023	4 ABL02624	Abk92192 Prostate	
C 11	39.6	7.8	1167	6 ABK92192	Abk92192 Prostate	
C 12	39.6	7.8	5643	6 ABK92193	Abk92193 Human prostatic acid phosphatase	
C 13	37.2	7.3	2712	8 ACA36793	ACA36793 Prokaryot	
C 14	37.2	7.3	110000	6 ABA03041	Continuation (19 o f)	
C 15	36.8	7.3	362	14 ADV77137	Adv77137 Huntingto n disease gene	
C 16	36.8	7.3	204803	12 ADG97348	Adq97348 Mouse can	
C 17	36	7.1	728	6 ABQ68881	ABQ68881 Listeria	
C 18	36	7.1	1296	6 ABQ67797	ABQ67797 Listeria	
C 19	36	7.1	1311	6 ABQ67800	ABQ67800 Listeria	

ALIGNMENTS

RESULT 1	XX	AAZ20010
ID ADZ89042	XX	AAZ89042 Standard; DNA; 507 BP.
AC AD289042;	XX	
DT 28-JUL-2005	XX	(first entry)
XX	DE	Pig growth factor I (GF V) gene, seq id 5.
XX	KW	Growth; biochip; swine; hog raising; growth factor V; gene; ds.
XX	OS	Sus scrofa; Kagoshima Berkshire.
XX	PN	US2005112597-A1.
XX	XX	
PD 26-MAY-2005.	XX	
PF 26-FEB-2004;	XX	2004US-00785981.
PR 24-NOV-2003;	XX	2003KR-00083653.
PA (KIMC/)	PA	KIM C.
PA (YEONJ/)	PA	YEO J.
PA (LEEFJ/)	PA	LEE J.
PA (SONG/)	PA	SONG Y.
PA (CHOK/)	PA	CHO K.
PA (CHUN/)	PA	CHUNG K.
PA (KIMI/)	PA	KIM I.
PA (JINS/)	PA	JIN S.
PA (PARK/)	PA	PARK S.
PA (JUNG/)	PA	JUNG J.
PA (LEE/)	PA	LEE M.
PA (KWON/)	PA	KWON E.
PA (CHOE/)	PA	CHO E.
PA (CHOH/)	PA	CHO H.
PA (SHIN/)	PA	SHIN S.
PA (NAMH/)	PA	NAM H.
PA (HONG/)	PA	HONG Y.
PA (HONG/)	PA	HONG S.
PA (KANG/)	PA	KANG Y.
PA (HAYX/)	PA	HAY X.

Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
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c	27	38.6	7.6	7.6	CD489728	CD489728 T27_D06_T		
c	28	38.6	7.6	7.6	BH211305	BH211305 Sm1-50G22		
c	29	38.6	7.6	7.6	AQ977896	AQ977896 RPCL-23-3		
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c	32	38.6	7.6	7.6	CO445036	CO445036 MZCCL1007		
c	33	38.6	7.6	7.6	CO446224	CO446224 MZCCL1009		
c	34	38.6	7.6	7.6	CO463295	CO463295 MZCCS1503		
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c	40	38.4	7.6	7.6	CFB39520	CFB39520 PBHB002xH		
c	41	38.4	7.6	7.6	CFB40809	CFB40809 PBHB010xO		
c	42	38.4	7.6	7.6	CFB64916	CFB64916 PBZP013xG		
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ALIGNMENTS

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LOCUS BX432596 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0D032YF14 3'-PRIME, mRNA sequence.

ACCESSION BX432596
VERSION BX432596.1 GI:30779118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;

REFERENCE 1 (bases 1 to 932)
AUTHORS Li W.B., Gruber C., Jesse J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 3874_r.
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?seq=CS0BAH0092B10NP1&c=3874_r.
Location/Qualifiers 1..932
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/note="Organ: brain Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."

FEATURES

1..932

1. .932

2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 3874_r.
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?seq=CS0BAH0092B10NP1&c=3874_r.
Location/Qualifiers 1..932
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Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ORIGIN

Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 11	34	6.7	1879	3	US-08-510-646B-5		Sequence 5, Appli
C 12	34	6.7	1879	3	US-09-231-818-5		Sequence 5, Appli
C 13	34	6.7	1879	3	US-09-635-359B-5		Sequence 5, Appli
C 14	33.8	6.7	1294	3	US-09-312-038-4		Sequence 4, Appli
C 15	33.8	6.7	1294	3	US-09-850-964-4		Sequence 4, Appli
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C 17	33.8	6.7	2289	3	US-09-510-964-3		Sequence 3, Appli
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C 19	33.2	6.5	567	4	US-09-605-703B-1299		Sequence 4, Appli
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C 23	32.4	6.4	2689	2	US-08-465-795-2		Sequence 2, Appli
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ALIGNMENTS

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 US-07-814-220-3/C

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; Sequence 3, Application US/07814220
; Patent No. 5925540
; GENERAL INFORMATION:
; APPLICANT: Caceci, Thomas B.
; APPLICANT: Toth, Thomas B.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Int'l. Center, 11800 Sunrise Valley Dr.
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,220
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael R.
; REGISTRATION NUMBER: 32,635
; REFERENCE DOCKET NUMBER: CIT.016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYP: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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Page 2

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RESULT 2
RS-07-812-421-3/C
Sequence 3 Application US/07812421
Patent No. 5932697

GENERAL INFORMATION:

APPLICANT: Caceci, Thomas E.
APPLICANT: Roth, Thomas E.
APPLICANT: Szumanski, Maria B. W.

TITLE OF INVENTION: SYNTHETIC AND
TITLE OF INVENTION: SYNTHETIC GENETIC
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WILSON
STREET: Boston Int'l. Center, 1
SUITE: Suite 900
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02191

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/812,
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/588,
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT 0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCUS: 31..324
RS-07-812-421-3/C

RESULT 3

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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5	61	12.0	523	7	US-10-785-981-5 Sequence 792.62, A	
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C	7	48.4	9.5	520	5	US-10-785-981-5 Sequence 332, Appli
C	8	39.8	7.9	5052	10	US-11-097-143-1178 Sequence 1178, AP
C	9	39.8	7.9	5023	10	US-11-097-143-1177 Sequence 1177, AP
C	10	39.6	7.8	5059	7	US-10-424-599-134445 Sequence 134445, AP
C	11	39.6	7.8	5643	6	US-10-012-952A-43 Sequence 43, Appli
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C	14	38	7.5	1052	10	US-10-437-963-1319 Sequence 1319, AP
C	15	37.2	7.3	2712	7	US-10-282-122A-24663 Sequence 24663, A
C	16	36.6	7.2	610	7	US-10-437-963-68546 Sequence 68546, A
C	17	36.6	7.2	1888	7	US-10-437-963-73429 Sequence 73429, A
C	18	36	7.1	728	7	US-10-398-221-1694 Sequence 1694, AP
C	19	36	7.1	1296	7	US-10-398-221-610 Sequence 610, AP
C	20	36	7.1	1311	7	US-10-398-221-613 Sequence 613, AP
C	21	36	7.1	2034	7	US-10-398-221-7 Sequence 615, AP
C	22	36	7.1	319630	7	US-10-398-221-7 Sequence 7, Appli
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ALIGNMENTS

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 ; Sequence 5, Application US/10785981
 ; Publication No. US20050112597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GYBONGSANGNAM-DO
 ; ATTORNEY OR AGENT: CHULWOOK, KIM
 ; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
 ; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
 ; FILE REFERENCE: 3884-0120P
 ; CURRENT APPLICATION NUMBER: US/10/785, 981
 ; CURRENT FILING DATE: 2004-06-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SBQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 5
 ; LENGTH: 507
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire

US-10-785-981-5
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Copyright GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.

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Run on: February 20, 2006, 11:27:30 ; Search time 387.381 Seconds
(without alignments)

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SUMMARIES

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c 8	32	6.3	2223	8	US-10-467-657-62265 Sequence 62265, AP
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c 18	31	6.1	889	12	US-11-136-527-3733 Sequence 373, AP
c 19	31	6.1	889	12	US-11-136-527-4469 Sequence 4469, AP
c 20	31	6.1	2183	9	US-11-072-512-1064 Sequence 1064, AP

ALIGNMENTS

RESULT 1
US-11-052-554A-520
; Sequence 520, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SBQ ID NO 520
; LENGTH: 3990
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
; US-11-052-554A-520

Query 358 CGGGGACTAGAACCCGTGTTGACGGTAAAGCTCATGGTAGCGCTGGGACCC 417 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 240456 ; LENGTH: 523 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-240456

Query 3288 AGGGGCAAGGGCGAACGGGCCAACCGGCCAACGGCCATACGGGACCC 3347

Query 4118 CGGTGTAAGCAGCTTACTACATGTTAGTTCAAGAACCCCTGCACATAC 477

Db 3348 CGGGGGACGGGACACGGGACACGGGACACGGGACACGGGACACGGGAC 3407

RESULT 2 US-11-136-527-2523

Db Sequence 2523, Application US/11136527

Db GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031986-01000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

PRIOR FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO: 2523

LENGTH: 2523

TYPE: DNA

ORGANISM: Rattus norvegicus

US-11-136-527-2523

Query Match 6.4%; Score 32.2; DB 12; Length 2539;

Best Local Similarity 40.6%; Pred. No. 4.7; Indels 0; Gaps 0;

Matches 85; Conservative 1; Mismatches 89;

Db 326 TTCCCCGATGCCCGCTTTACACCATCGGGACTAGAACCGTTGGTCAGC 385

Db 431 TCCCCCAGGAGCCCTCCGGGACCCCTGCTGGAGCTCCGAGCTTCAGCG 490

Query 386 GTAGGGCTATGGAGCTGTGGCGACGCCCTGTACCGCTTACTACATGTTAGT 445

Db 491 AGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 550

Query 446 TTCAAGAACACCCCTGCCATAACCGGTGTCCTACTCCAACTCTGGTTCA 500

Db 551 CCCTGCCCTAGCTGCCAACTCCAGGCAAGSTTGCCATCCCTGGCA 605

RESULT 3 US-09-925-065A-240456

Sequence 240456, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 09/925-065A-461295

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 108827.135

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 108827.135

LENGTH: 617

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-461295

Query Match 6.3%; Score 32; DB 6; Length 617;

Best Local Similarity 48.9%; Pred. No. 3.9; Indels 0; Gaps 0;

Matches 86; Conservative 0; Mismatches 90;

Db 44 CCAGAACACGGCAACCTAGGGATTATAAATAGGTATAAGCCATAC 103

Db 10 CAAATCCATGGCTGGCTGGAGCTGAGGTGAAGCTGGCCCTATGCTGAGCTCAATTAAG 345

Query 104 TCACTACCCGAAACGGGACACTAGGGCTCCGCATAAGCCATCCCTTCCTGGTCGTC 163

Db 346 CAGCTTAAGGAGGAGGAGAAACCTTACGGCTCCAGAGGAGCCCTTCCTGCTGATAATA 405

Query 164 GATGTTGGGGCTGAGTATAGGCTTCCAAACGCTTACCGCCA 219

Db 406 CCAGCTCAGGATAACTCTGTAAGGAGTCATTGCTGAAACAATCTGAGGCCA 461

RESULT 4 US-09-925-065A-461295

Sequence 461295, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925-065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 108827.135

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 108827.135

LENGTH: 617

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-461295

Query Match 6.3%; Score 32; DB 6; Length 617;

Best Local Similarity 48.9%; Pred. No. 3.9; Indels 0; Gaps 0;

Matches 86; Conservative 0; Mismatches 90;

Db 44 CCAGAACACGGCAACCTAGGGATTATAAATAGGTATAAGCCATAC 103

Db 10 CAAATCCATGGCTGGCTGGAGCTGAGGTGAAGCTGGCCCTATGCTGAGCTCAATTAAG 345

Query 104 TCACTACCCGAAACGGGACACTAGGGCTCCGCATAAGCCATCCCTTCCTGGTCGTC 163

Db 70 CAGCTTAAGGAGGAGGAGAAACCTTACGGCTCCAGAGGAGCCCTTCCTGCTGATAATA 129

Query 164 GATGTTGGGGCTGAGTATAGGCTTCCAAACGCTTACCGCCA 219

Db 130 CCAGCTCAGGATAACTCTGTAAGGAGTCATTGCTGAAACAATCTGAGGCCA 185

RESULT 5 US 11-120 061-930

Sequence 930, Application US/11128061